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(54) Title: COMPOSITIONS FROM THE GRASSES *LOLIUM PERENNE* AND *FESTUCA ARUNDINACEA*

(57) Abstract: Isolated polynucleotides encoding polypeptides from *Lolium perenne* and *Festuca arundinacea* active in lignin, fructan and tannin biosynthetic pathways are provided, together with expression vector and host cells comprising such isolated polynucleotides. Methods for the use of such polynucleotides and polypeptides are also provided.



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Compositions from the grasses *Lolium perenne* and *Festuca arundinacea*.

**COMPOSITIONS ISOLATED FROM FORAGE GRASSES
AND METHODS FOR THEIR USE**

Reference to Related Applications

This application claims priority to U.S. Provisional Patent Application No. 60/337,703 filed November 7, 2001.

Technical Field of the Invention

This invention relates to polynucleotides isolated from forage grass tissues, specifically from *Lolium perenne* (perennial ryegrass) and *Festuca arundinacea* (tall fescue), as well as oligonucleotide probes and primers, genetic constructs comprising the polynucleotides, biological materials (including host cells and plants) incorporating the polynucleotides, polypeptides encoded by the polynucleotides, and methods for using the polynucleotides and polypeptides. More particularly, the invention relates to polypeptides involved in the lignin, tannin and fructan biosynthetic pathways, and to polynucleotides encoding such polypeptides.

Background of the Invention

Over the past 50 years, there have been substantial improvements in the genetic production potential of ruminant animals (sheep, cattle and deer). Levels of meat, milk or fiber production that equal an animal's genetic potential may be attained within controlled feeding systems, where animals are fully fed with energy dense, conserved forages and grains. However, the majority of temperate farming systems worldwide rely on the *in situ* grazing of pastures. Nutritional constraints associated with temperate pastures can prevent the full expression of an animal's genetic potential. This is illustrated by a comparison between milk production by North American grain-fed dairy cows and New Zealand pasture-fed cattle. North American dairy cattle produce, on average, twice the milk volume of New Zealand cattle, yet the genetic base is similar within both systems (New Zealand Dairy Board and United States Department of Agriculture figures). Significant potential therefore exists

to improve the efficiency of conversion of pasture nutrients to animal products through the correction of nutritional constraints associated with pastures.

Lignin Biosynthetic Pathway

5 Lignin is an insoluble polymer that serves as a matrix around the polysaccharide components of some plant cell walls, and that is primarily responsible for the rigidity of plant stems. Generally, the higher the lignin content, the more rigid the plant. For example, tree species synthesize large quantities of lignin, with lignin constituting 20%-30% of the dry weight of wood. The lignin content of grasses ranges from 2-8% of dry weight and changes
10 during the growing season. In addition to providing rigidity, lignin aids in water transport within plants by rendering cell walls hydrophobic and water impermeable. Lignin also plays a role in disease resistance of plants by impeding the penetration and propagation of pathogenic agents.

 Forage digestibility is affected by both lignin composition and concentration. Lignin
15 is largely responsible for the digestibility, or lack thereof, of forage crops, with small increases in plant lignin content resulting in relatively high decreases (> 10%) in digestibility (Buxton and Russell, *Crop. Sci.* 28:5358-558, 1988). For example, crops with reduced lignin content provide more efficient forage for cattle, with the yield of milk and meat being higher relative to the amount of forage crop consumed. During normal plant growth, an increase in
20 the maturity of the plant stem is accompanied by a corresponding increase in lignin content and composition that causes a decrease in digestibility. This change in lignin composition is to one of increasing syringyl:guaiacyl (S:G) ratio. When deciding on the optimum time to harvest forage crops, farmers must therefore choose between a high yield of less digestible material and a lower yield of more digestible material.

25 Lignin is formed by polymerization of three different monolignols, *para*-coumaryl alcohol, coniferyl alcohol and sinapyl alcohol, that are synthesized in a multistep pathway, with each step in the pathway being catalyzed by a different enzyme. The three monolignols are derived from phenylalanine or tyrosine in a multistep process and are then polymerized into lignin by a free radical mechanism. Following polymerization, *para*-coumaryl alcohol,
30 coniferyl alcohol and sinapyl alcohol are converted into the *p*-hydroxyphenyl (H), guaiacyl (G) and syringyl (S) units of lignin, respectively. While these three types of lignin subunits

are well known, it is likely that slightly different variants of these subunits may be involved in the lignin biosynthetic pathway in various plants. For example, studies suggest that both free monolignols and monolignol-4-coumarate esters may be substrates for lignin formation in grasses. The relative concentration of the monolignol residues in lignin varies among different plant species and within species. For example, the monolignol content for H/G/S of grasses, alfalfa and softwood gymnosperms is 22%/44%/34%, 7%/39%/54% and 14%/80%/6%, respectively (van Soest in "Nutritional Ecology of the Ruminant". Cornell University Press, Ithaca, NY). The composition of lignin may also vary among different tissues within a specific plant.

Coniferyl alcohol, *para*-coumaryl alcohol and sinapyl alcohol are synthesized by similar pathways (Whetten *et al.*, *Annu. Rev. Plant Physiol. Plant Mol. Biol.* 49:585-609, 1998; Guo *et al.*, *Plant Cell* 13:73-88, 2001). The first step in the lignin biosynthetic pathway is the deamination of phenylalanine or tyrosine by phenylalanine ammonia-lyase (PAL) or tyrosine ammonia-lyase (TAL), respectively. In maize, the PAL enzyme also has TAL activity (Rosler *et al.*, *Plant Physiol.* 113:175-179, 1997). The product of TAL activity on tyrosine is 4-coumarate, whereas the product of PAL activity on phenylalanine is cinnamate which is then hydroxylated by cinnamate 4-hydroxylase (C4H) to form 4-coumarate. 4-Coumarate is hydroxylated by coumarate 3-hydroxylase (C3H) to give caffeate. The newly added hydroxyl group is then methylated by caffeic acid O-methyl transferase (COMT) to give ferulate. Several other methylation reactions can be catalyzed by COMT, including caffeoylaldehyde to coniferaldehyde, and 5-hydroxyconiferaldehyde to sinapaldehyde. 4-Coumarate, caffeate and ferulate can all be conjugated to coenzyme A by 4-coumarate:CoA ligase (4CL) to form 4-coumaryl CoA, caffeoyl CoA and feruloyl CoA, respectively. Caffeoyl CoA can then be methylated by the enzyme caffeoyl-CoA O-methyl transferase (CAMT).

Coniferaldehyde is hydroxylated to 5-hydroxyconiferaldehyde by ferulate 5-hydroxylase (F5H). Reduction of 4-coumaryl CoA, caffeoyl CoA and feruloyl-CoA to 4-coumaraldehyde, caffeoyl aldehyde and coniferaldehyde, respectively, is catalyzed by cinnamoyl-CoA reductase (CCR). Coumaraldehyde, caffeoyl aldehyde, coniferaldehyde and 5-hydroxyconiferaldehyde are further reduced by the action of cinnamyl alcohol dehydrogenase (CAD) to give coniferyl alcohol which is then converted into its glucosylated

form for export from the cytoplasm to the cell wall by coniferol glucosyl transferase (CGT). Recently a sinapyl alcohol dehydrogenase (SAD) was described that converts sinapaldehyde to sinapyl alcohol (Li *et al.*, *Plant Cell* 13:1567-1586, 2001). Following export, the de-glucosylated form of coniferyl alcohol is obtained by the action of coniferin *beta*-glucosidase (CBG). Finally, polymerization of the three monolignols to provide lignin is catalyzed by phenolase (PNL), laccase (LAC) and peroxidase (PER). For a more detailed review of the lignin biosynthetic pathway, see Whetton R and Sederoff R, *The Plant Cell*, 7:1001-1013, 1995 and Whetten *et al.*, *Annu. Rev. Plant Physiol. Plant Mol. Biol.* 49:585-609, 1998.

Both lignin levels and composition have been changed in a range of plant species by altering the expression of specific lignin biosynthetic enzymes. For example, anti-sense 4CL constructs in transgenic aspen trees reduced lignin content from 20 to 11% (a 45% reduction) but at the same time increased both cellulose levels (by 15%) and growth rate (Hu *et al.* *Nature Biotechnol.* 17:808-812, 1999). These trees had the same level of total carbon, suggesting that carbon partitioning had been altered. Reducing 4CL by either anti-sense or sense-suppression in tobacco plants led to an accumulation of hydroxycinnamic acids in cell walls as well as a reduction in both guaiacyl and syringyl lignin units (Kajita *et al.*, *Plant Cell. Physiol.* 37:957-965, 1996). In transgenic tobacco plants in which levels of C4H were reduced by anti-sense or sense suppression, total lignin content was reduced, in addition to a reduction in syringyl lignin units (Sewalt *et al.*, *Plant Physiol.* 115:41-50, 1997). Reducing the levels of PAL in tobacco plants by anti-sense or sense-suppression reduced total lignin content but did not change the syringyl-guaiacyl (S:G) lignin ration. In alfalfa, reducing expression of COMT through either anti-sense or gene silencing decreased total lignin by decreasing the amount of guaiacyl units and resulted in a near total loss of syringyl lignin units (Guo *et al.*, *Plant Cell* 13:73-88, 2001). In contrast, reducing CCOMT expression through anti-sense or gene silencing in alfalfa plants also decreased total lignin by reducing the total amount of guaiacyl lignin units but had no effect on the amount of syringyl lignin. Reducing CCR expression by anti-sense in tobacco plants resulted in reduced lignin content and increased S:G ratios due to lower guaiacyl lignin units (Piquemal *et al.*, *Plant J.* 13:71-83, 1998). *A. thaliana* plants where the F5H gene had been mutated contained only traces of syringyl lignin (Marita *et al.*, *Proc. Natl. Acad. Sci. USA* 96:12323-12332, 1999).

Alteration of grass lignin composition may usefully be employed to maintain high forage digestibility throughout the year. This is most important when the plant is approaching flowering and/or during flowering. At this time, the entire lignin biosynthetic pathway will preferably be reduced, in particular lowering the amount of syringyl lignin units, thereby lowering the S:G ratio and maintaining the digestibility of the forage crop.

Several of the enzymes involved in the lignin biosynthetic pathway also have other functions within the plant. For example, PAL is a key enzyme of plant and fungi phenylpropanoid metabolism and catalyzes the first step in phenylpropanoid metabolism. It is involved in the biosynthesis of a wide variety of secondary metabolites such as flavonoids, furanocoumarin in phytoalexins and cell wall components. These compounds have many important roles in plants during normal growth and in responses to environmental stress. PAL catalyzes the removal of an ammonia group from phenylalanine to form trans-cinnamate. PAL and the related histidine ammonia lyase are unique enzymes which are known to have the modified amino acid dehydroalanine (DHA) in their active site (Taylor *et al.*, *J. Biol. Chem.* 265:18192-18199, 1990). Phenylalanine and histidine ammonia-lyases (PAL) active site has a consensus of GTITASGDLVPLSYIA. The serine residue is central to the active site, and the region around this active site residue is well conserved (Langer *et al.*, *Biochem.* 33:6462-6467, 1994).

C4H, which is a member of the cytochrome P450 monooxygenase superfamily, plays a central role in both phenylpropanoid metabolism and lignin biosynthesis where it anchors a phenylpropanoid enzyme complex to the endoplasmic reticulum (ER). The phenylpropanoid pathway controls the synthesis of lignin, flower pigments, signaling molecules, and a large spectrum of compounds involved in plant defense against pathogens and UV light. This is also a branch point between general phenylpropanoid metabolism and pathways leading to various specific end products. 4CLs are a group of enzymes necessary for maintaining a continuous metabolic flux for the biosynthesis of plant phenylpropanoids, such as lignin and flavonoids that are essential to the survival of plants, because they serve important functions in plant growth and adaptation to environmental perturbations. Three isoforms of 4CL have been identified with distinct substrate preference and specificities. Expression studies in angiosperms revealed a differential behavior of the three genes in various plant organs and upon external stimuli such as wounding and UV irradiation or upon challenge with fungi.

One isoform is likely to participate in the biosynthetic pathway leading to flavonoids whereas the other two are probably involved in lignin formation and in the production of additional phenolic compounds other than flavonoids (Ehlting *et al.*, *Plant J.* 19:9-20, 1999).

F5H is involved in the phenylpropanoid biosynthesis pathway. It belongs to the CYP84 subfamily of the cytochrome P450 family and is known as cytochrome P450 84A1. F5H is one of the enzymes in the pathways leading to the synthesis of sinapic acid esters, but also has coniferaldehyde hydroxylase activity (Nair *et al.*, *Plant Physiol.* 123:1623-1634, 2000). In the generalized pathway for phenylpropanoid metabolism, F5H catalyzes the formation of 5-hydroxyferulate (a precursor of sinapate) and sinapate in turn as the precursor for sinapine and for sinapoyl CoA in two bifurcated pathways (Chapple *et al.*, *Plant Cell* 4:1413-1424, 1992). Sinapoyl CoA has been considered as the precursor for sinapyl alcohol, which is then polymerized into syringyl (S) lignin. In addition, CYP84 F5H product carries out the hydroxylation of coniferaldehyde (ConAld) to 5-OH ConAld (Nair *et al.*, *Plant Physiol.* 123:1623-1634, 2000).

Peroxidases are heme-containing enzymes that use hydrogen peroxide as the electron acceptor to catalyze a number of oxidative reactions. They belong to a superfamily consisting of 3 major classes. Class III consists of the secretory plant peroxidases, which have multiple tissue-specific functions in removal of hydrogen peroxide from chloroplasts and cytosol, oxidation of toxic compounds, biosynthesis of the cell wall, defense responses towards wounding, indole-3-acetic acid (IAA) catabolism and ethylene biosynthesis.

Fructan Biosynthetic Pathway

Plant carbohydrates can be divided into two groups depending on their function within the plant. Structural carbohydrates, such as cellulose, are usually part of the extracellular matrix. Non-structural, storage carbohydrates act as either long- or short-term carbohydrate stores. Examples of non-structural carbohydrates include starch, sucrose and fructans.

Fructans are polymers that are stored in the vacuole and that consist of linear and branched chains of fructose units (for review see Vijn and Smeekens *Plant Physiol.* 120:351-359, 1999). They play an important role in assimilate partitioning and possibly in stress tolerance in many plant families. Grasses use fructans instead of starch as a water-soluble

carbohydrate store (Pollock *et al.*, in "Regulation of primary metabolic pathways in plants", N.J. Kruger *et al.*, (eds), Kluwer Academic Publishers, The Netherlands, pp195-226, 1999). Increasing the amount of fructans and sucrose in forage crops leads to an increase in the level of water-soluble carbohydrates and thereby enhances the nutritional value of the plants. In addition, increasing the amount of fructans in forage plants decreases methane production in animals fed the plants, thereby leading to lower greenhouse gas emissions, and decreases urea production in animals as less protein is degraded in the rumen (Biggs and Hancock, *Trends in Plant Sci.* 6:8-9, 2001). Fructans have also been implicated in protecting plants against water deficits caused by drought or low temperatures. Introduction of enzymes involved in the fructan biosynthetic pathway into plants that do not naturally synthesize fructans may be employed to confer cold tolerance and drought tolerance (Pilon-Smits, *Plant Physiol.* 107:125-130, 1995).

The number of fructose units within a fructan chain is referred to as the degree of polymerization (DP). In grasses, fructans of DP 6-10 are common. Such fructans of low DP are naturally sweet and are therefore of interest for use as sweeteners in foodstuffs. Long fructan chains form emulsions with a fat-like texture and a neutral taste. The human digestive system is unable to degrade fructans, and fructans of high DP may therefore be used as low-calorie food ingredients. Over-expression of enzymes involved in the fructan biosynthetic pathway may be usefully employed to produce quantities of fructans that can be purified for human consumption.

Five major classes of structurally different fructans have been identified in plants, with each class showing a different linkage of the fructosyl residues. Fructans found in grasses are of the mixed levan class, consisting of both (2-1)- and (2-6)-linked beta-D-fructosyl units (Pollock *et al.*, in "Regulation of primary metabolic pathways in plants", N.J. Kruger *et al.*, (eds), Kluwer Academic Publishers, The Netherlands, pp195-226, 1999). Fructans are synthesized by the action of fructosyltransferase enzymes on sucrose in the vacuole. These enzymes are closely related to invertases, enzymes that normally hydrolyze sucrose.

Grasses use two fructosyltransferase enzymes to synthesize fructans, namely sucrose:sucrose 1-fructosyltransferase (1-SST) and sucrose:fructan 6-fructosyltransferase (6-SFT) (Pollock *et al.*, in "Regulation of primary metabolic pathways in plants", N.J. Kruger *et*

al., (eds), Kluwer Academic Publishers, The Netherlands, pp195-226, 1999). 1-SST is a key enzyme in plant fructan biosynthesis, while 6-SFT catalyzes the formation and extension of beta-2,6-linked fructans that is typically found in grasses. Specifically, 1-SST catalyzes the formation of 1-kestose plus glucose from sucrose, while 6-SFT catalyzes the formation of bifurcose plus glucose from sucrose plus 1-kestose and also the formation of 6-kestose plus glucose from sucrose. Both enzymes can modify 1-kestose, 6-kestose and bifurcose further by adding additional fructose molecules. Over-expression of both 1-SST and 6-SFT in the same plant may be employed to produce fructans for use in human foodstuffs (Sevenier *et al.*, *Nature Biotechnol.* 16:843-846; Hellwege *et al.*, *Proc. Nat. Acad. Sci. USA* 97:8699-8704, 2000).

The synthesis of sucrose from photosynthetic assimilates in plants, and therefore the availability of sucrose for use in fructan formation, is controlled, in part, by the enzymes sucrose phosphate synthase (SPS) and sucrose phosphate phosphatase (SPP). Sucrose plays an important role in plant growth and development, and is a major end product of photosynthesis. It also functions as a primary transport sugar and in some cases as a direct or indirect regulator of gene expression (for a review see Smeekens, *Curr. Opin. Plant Biol.* 1:230-234, 1998). SPS regulates the synthesis of sucrose by regulating carbon partitioning in the leaves of plants and therefore plays a major role as a limiting factor in the export of photoassimilates out of the leaf. The activity of SPS is regulated by phosphorylation and moderated by concentration of metabolites and light (Huber *et al.*, *Plant Physiol.* 95:291-297, 1991). Specifically, SPS catalyzes the transfer of glucose from UDP-glucose to fructose-6-phosphate, thereby forming sucrose-6-phosphate (Suc-6-P). Suc-6-P is then dephosphorylated by SPP to form sucrose (Lunn *et al.*, *Proc. Natl. Acad. Sci. USA* 97:12914-12919, 2000). The enzymes SPS and SPP exist as a heterotetramer in the cytoplasm of mesophyll cells in leaves, with SPP functioning to regulate SPS activity. SPS is also important in ripening fruits, sprouting tubers and germinating seeds (Laporte *et al.*, *Planta* 212:817-822, 2001).

Once in the vacuole, sucrose can be converted into fructan by fructosyltransferases as discussed above, or hydrolyzed into glucose and fructose by the hydrolase enzymes known as invertases (Sturm, *Plant Physiol.* 121:1-7, 1999). There are several different types of invertases, namely extracellular (cell wall), vacuolar (soluble acid) and cytoplasmic, with at

least two isoforms of each type of invertase normally being found within a plant species. In addition to having different subcellular locations, the different types of invertases have different biochemical properties. For example, soluble and cell wall invertases operate at acidic pH, whereas cytoplasmic invertases work at a more neutral or alkaline pH. Invertases are believed to regulate the entry of sucrose into different utilization pathways (Grof and Campbell, *Aust. J. Plant Physiol.* 28:1-12, 2001). Reduced invertase activity may increase the level of water-soluble carbohydrates in plants. Plants contain several isoforms of cell wall invertases (CWINV), which accumulate as soluble proteins. CWINV plays an important role in phloem unloading and in stress response. It hydrolyzes terminal non-reducing beta-D-fructofuranoside residues in beta-D-fructo-furanosides.

Another enzyme that acts upon sucrose in plants is soluble sucrose synthase (SUS). Recent results indicate that SUS is localized in the cytosol, associated with the plasma membrane and the actin cytoskeleton. Phosphorylation of SUS is one of the factors controlling localization of the enzyme (Winter and Huber, *Crit. Rev. Biochem. Mol. Biol.* 35:253-89, 2000). It catalyzes the transfer of glucose from sucrose to UDP, yielding UDP-glucose and fructose. Increasing the amount of SUS in a plant increases the amount of cellulose synthesis, whereas decreasing SUS activity should increase fructan levels. Increased SUS concentration may also increase the yield of fruiting bodies. SUS activity is highest in carbon sink tissues in plants and low in photosynthetic source tissues, and studies have indicated that SUS is the main sucrose-cleaving activity in sink tissues. Grasses have two isoforms of SUS that are encoded by separate genes. These genes are differentially expressed in different tissues.

Tannin Biosynthetic Pathway

Condensed tannins are polymerized flavonoids. More specifically, tannins are composed of catechin 4-ol and catechin monomer units, and are stored in the vacuole. In many temperate forage crops, such as ryegrass and fescue, foliar tissues are tannin-negative. This leads to a high initial rate of fermentation when these crops are consumed by ruminant livestock, resulting in both protein degradation and production of ammonia by the livestock. These effects can be reduced by the presence of low to moderate levels of tannin. In certain other plant species, the presence of high levels of tannins reduces palatability and nutritive

value. Introduction of genes encoding enzymes involved in the biosynthesis of condensed tannins into a plant may be employed to synthesize flavonoid compounds that are not normally made in the plant. These compounds may then be isolated and used for treating human or animal disorders or as food additives.

5 Much of the biosynthetic pathway for condensed tannins is shared with that for anthocyanins, which are pigments responsible for flower color. Therefore, modulation of the levels of enzymes involved in the tannin biosynthetic pathway may be employed to alter the color of foliage and the pigments produced in flowers.

10 Most tannins described to date contain pro-cyanidin units derived from dihydroquercetin and pro-delphinidin units derived from dihydromyricetin. However, some tannins contain pro-pelargonidin units derived from dihydrokaempferol. The initial step in the tannin biosynthetic pathway is the condensation of coumaryl CoA with malonyl CoA to give naringenin-chalcone, which is catalyzed by the enzyme chalcone synthase (CHS). The enzyme chalcone isomerase (CHI) catalyzes the isomerization of naringenin chalcone to
15 naringenin (also known as flavanone), which is then hydroxylated by the action of the enzyme flavonone 3- β -hydroxylase (F3 β H) to give dihydrokaempferol. The enzyme flavonoid 3'-hydroxylase (F3'OH) catalyzes the conversion of dihydrokaempferol to dihydroquercetin, which in turn can be converted into dihydromyricetin by the action of flavonoid 3'5'-hydroxylase (F3'5'OH). The enzyme dihydroflavonol-4-reductase (DFR)
20 catalyzes the last step before dihydrokaempferol, dihydroquercetin and dihydromyricetin are committed for either anthocyanin (flower pigment) or proanthocyanidin (condensed tannin) formation. DFR also converts dihydrokaempferol to afzelchin-4-ol, dihydroquercetin to catechin-4-ol, and dihydromyricetin to gallocatechin-4-ol, probably by the action of more than one isoform. For a review of the tannin biosynthetic pathway, see, Robbins M.P. and
25 Morris P. in *Metabolic Engineering of Plant Secondary Metabolism*, Verpoorte and Alfermann (eds), Kluwer Academic Publishers, the Netherlands, 2000.

30 While polynucleotides encoding some of the enzymes involved in the lignin, fructan and tannin biosynthetic pathways have been isolated for certain species of plants, genes encoding many of the enzymes in a wide range of plant species have not yet been identified.

Thus there remains a need in the art for materials useful in the modification of lignin, fructan and tannin content and composition in plants, and for methods for their use.

Summary of the Invention

5 The present invention provides enzymes involved in the lignin, fructan or tannin biosynthetic pathways that are encoded by polynucleotides isolated from forage grass tissues. The polynucleotides were isolated from *Lolium perenne* (perennial ryegrass) and *Festuca arundinacea* (tall fescue) tissues taken at different times of the year, specifically in winter and spring, and from different parts of the plants, including: leaf blades, leaf base,
10 pseudostems, floral stems, roots, inflorescences and stems. The present invention also provides genetic constructs, expression vectors and host cells comprising the inventive polynucleotides, and methods for using the inventive polynucleotides and genetic constructs to modulate the biosynthesis of lignins, fructans and tannins.

 In specific embodiments, the isolated polynucleotides of the present invention
15 comprise a sequence selected from the group consisting of: (a) SEQ ID NO: 1-62 and 125-162; (b) complements of SEQ ID NO: 1-62 and 125-162; (c) reverse complements of SEQ ID NO: 1-62 and 125-162; (d) reverse sequences of SEQ ID NO: 1-62 and 125-162; (e) sequences having a 99% probability of being functionally or evolutionarily related to a sequence of (a)-(d), determined as described below; and (f) sequences having at least 75%,
20 80%, 90% or 98% identity to a sequence of (a)-(d), the percentage identity being determined as described below. Polynucleotides comprising at least a specified number of contiguous residues ("x-mers") of any of SEQ ID NO: 1-62 and 125-162; and oligonucleotide probes and primers corresponding to SEQ ID NO: 1-62 and 125-162 are also provided. All of the above polynucleotides are referred to herein as "polynucleotides of the present invention."

25 In further aspects, the present invention provides isolated polypeptides comprising an amino acid sequence of SEQ ID NO: 63-124 and 163-190, together with polypeptides comprising a sequence having at least 75%, 80%, 90% or 98% identity to a sequence of SEQ ID NO: 63-124 and 163-190, wherein the polypeptide possesses the same functional activity as the polypeptide comprising a sequence of SEQ ID NO: 63-124 and 163-190. The present
30 invention also contemplates isolated polypeptides comprising at least a functional portion of a polypeptide comprising an amino acid sequence selected from the group consisting of: (a)

SEQ ID NO: 63-124 and 163-190; and (b) sequences having at least 75%, 80%, 90% or 98% identity to a sequence of SEQ ID NO: 63-124 and 163-190.

In another aspect, the present invention provides genetic constructs comprising a polynucleotide of the present invention, either alone, in combination with one or more of the inventive sequences, or in combination with one or more known polynucleotides.

In certain embodiments, the present invention provides genetic constructs comprising, in the 5'-3' direction: a gene promoter sequence; an open reading frame coding for at least a functional portion of a polypeptide of the present invention; and a gene termination sequence. An open reading frame may be orientated in either a sense or anti-sense direction. Genetic constructs comprising a non-coding region of a polynucleotide of the present invention or a polynucleotide sequence complementary to a non-coding region, together with a gene promoter sequence and a gene termination sequence, are also provided. Preferably, the gene promoter and termination sequences are functional in a host cell, such as a plant cell. Most preferably, the gene promoter and termination sequences are those of the original enzyme genes but others generally used in the art, such as the Cauliflower Mosaic Virus (CMV) promoter, with or without enhancers, such as the Kozak sequence or Omega enhancer, and *Agrobacterium tumefaciens* nopal synthase terminator may be usefully employed in the present invention. Tissue-specific promoters may be employed in order to target expression to one or more desired tissues. The construct may further include a marker for the identification of transformed cells.

In a further aspect, transgenic cells, such as transgenic plant cells, comprising the constructs of the present invention are provided, together with tissues and plants comprising such transgenic cells, and fruits, seeds and other products, derivatives, or progeny of such plants.

In yet another aspect, methods for modulating the lignin, fructan or tannin content and composition of a target organism, such as a plant, are provided, such methods including stably incorporating into the genome of the target plant a genetic construct comprising a polynucleotide of the present invention. In a preferred embodiment, the target plant is a forage grass, preferably selected from the group consisting of *Lolium* and *Festuca* species, and most preferably from the group consisting of *Lolium perenne* and *Festuca arundinacea*. In a related aspect, a method for producing a plant having altered lignin, fructan or tannin

composition is provided, the method comprising transforming a plant cell with a genetic construct comprising of the present invention to provide a transgenic cell, and cultivating the transgenic cell under conditions conducive to regeneration and mature plant growth.

In yet a further aspect, the present invention provides methods for modifying the activity of an enzyme in a target organism, such as a plant, comprising stably incorporating into the genome of the target organism a genetic construct of the present invention. In a preferred embodiment, the target plant is a forage grass, preferably selected from the group consisting of *Lolium* and *Festuca* species, and most preferably from the group consisting of *Lolium perenne* and *Festuca arundinacea*.

Brief Description of the Drawings

Fig. 1 shows the activity of recombinant LpSPP (SEQ ID NO: 8) and FaSPP (SEQ ID NO 7) on dephosphorylating Suc-6-P and Fru-6-P. The pET41a extract was the vector control.

Fig. 2 shows the peroxidase activity of PER3 (SEQ ID NO: 50) and PER5 (SEQ ID NO: 52) as determined by oxidation of ABTS. Horseradish peroxidase of known activity (Sigma, St Louis, MI) was used as a positive control and boiled samples as a negative control.

Fig. 3 shows PCR verification of transgenic *N. benthamiana* plants transformed with Lp6-SFT1 (SEQ ID NO: 3). Genomic DNA was isolated from kanamycin resistant T2 *N. benthamiana* plants and the Lp6-SFT fragment was amplified using specific PCR primers.

Fig. 4 shows PCR verification of transgenic *N. benthamiana* plants transformed with Lp1-SST (SEQ ID NO: 1). Genomic DNA was isolated from kanamycin resistant T2 *N. benthamiana* plants and the Lp1-SST fragment was amplified using specific PCR primers.

Plant number 5 is a non-transgenic control.

Fig. 5 shows the fructan level in transgenic *N. benthamiana* lines transformed with Lp6-SFT1 (SEQ ID NO: 3) and Lp1-SST (SEQ ID NO: 1).

Fig. 6 shows the sucrose synthesizing activity of FaSPS-N (SEQ ID NO: 9) with and without SPP (SEQ ID NO: 8) in mammalian cell extracts. The non-transfected cells are controls.

Fig. 7 shows the sucrose cleaving activity of FaSUS1 (SEQ ID NO: 13) in mammalian cell extracts.

Fig. 8 shows the invertase activity for vacuolar invertase (SEQ ID NO: 25) and two cell wall invertases (SEQ ID NO: 17 and 19); absence of invertase activity from an empty
5 vector (pPICZalphaA) control is also shown.

Detailed Description of the Invention

The polypeptides of the present invention, and the polynucleotides encoding the polypeptides, have activity in lignin, fructan and tannin biosynthetic pathways in plants.
10 Using the methods and materials of the present invention, the lignin, fructan and/or tannin content of a plant may be modulated by modulating expression of polynucleotides of the present invention, or by modifying the polynucleotides or polypeptides encoded by polynucleotides. The isolated polynucleotides and polypeptides of the present invention may thus be usefully employed in the correction of nutritional imbalances associated with
15 temperate pastures and to increase the yield of animal products from pastures.

The lignin, fructan and/or tannin content of a target organism, such as a plant, may be modified, for example, by incorporating additional copies of genes encoding enzymes involved in the lignin, fructan or tannin biosynthetic pathways into the genome of the target plant. Similarly, a modified lignin, fructan and/or tannin content can be obtained by
20 transforming the target plant with anti-sense copies of such genes. In addition, the number of copies of genes encoding for different enzymes in the lignin, fructan and tannin biosynthetic pathways can be manipulated to modify the relative amount of each monomer unit synthesized, thereby leading to the formation of lignins, fructans or tannins having altered composition.

25 The present invention thus provides methods for modulating the polynucleotide and/or polypeptide content and composition of an organism, such methods involving stably incorporating into the genome of the organism a genetic construct comprising one or more polynucleotides of the present invention. In one embodiment, the target organism is a plant species, preferably a forage plant, more preferably a grass of the *Lolium* or *Festuca* species,
30 and most preferably *Lolium perenne* or *Festuca arundinacea*. In related aspects, methods for producing a plant having an altered genotype or phenotype is provided, such methods

comprising transforming a plant cell with a genetic construct of the present invention to provide a transgenic cell, and cultivating the transgenic cell under conditions conducive to regeneration and mature plant growth. Plants having an altered genotype or phenotype as a consequence of modulation of the level or content of a polynucleotide or polypeptide of the present invention compared to a wild-type organism, as well as components (seeds, etc.) of such plants, and the progeny of such plants, are contemplated by and encompassed within the present invention.

The isolated polynucleotides of the present invention have utility in genome mapping, in physical mapping, and in positional cloning of genes. Additionally, the polynucleotide sequences identified as SEQ ID NOS: 1-62 and 125-162 and their variants, may be used to design oligonucleotide probes and primers. Oligonucleotide probes and primers have sequences that are substantially complementary to the polynucleotide of interest over a certain portion of the polynucleotide. Oligonucleotide probes designed using the polynucleotides of the present invention may be employed to detect the presence and examine the expression patterns of genes in any organism having sufficiently similar DNA and RNA sequences in their cells using techniques that are well known in the art, such as slot blot DNA hybridization techniques. Oligonucleotide primers designed using the polynucleotides of the present invention may be used for PCR amplifications. Oligonucleotide probes and primers designed using the polynucleotides of the present invention may also be used in connection with various microarray technologies, including the microarray technology of Affymetrix (Santa Clara, CA).

In a first aspect, the present invention provides isolated polynucleotide sequences identified in the attached Sequence Listing as SEQ ID NO: 1-62 and 125-162, and polypeptide sequences identified in the attached Sequence Listing as SEQ ID NO: 63-124 and 163-190. The polynucleotides and polypeptides of the present invention have demonstrated similarity to the following polypeptides that are known to be involved in lignin, fructan and tannin biosynthetic processes:

TABLE 1

SEQ ID NO Polynucleotide	SEQ ID NO Polypeptide	Category	Description
1 and 125	63 and 163	Fructan biosynthesis	Homolog of Sucrose:Sucrose 1-fructosyl-transferase (1-SST) isolated from <i>Festuca arundinacea</i> . They contain a typical signature of the glycosyl hydrolases family 32 (amino acid residues 120 to 133). The glycosyl hydrolases family 32 domain signature has a consensus of HYQPxxH/NxxNDPNG, where D is the active site residue (Henrissat, <i>Biochem. J.</i> 280:309-316, 1991).
2	64	Fructan biosynthesis	Homolog of Sucrose:Sucrose 1-fructosyl-transferase (1-SST) isolated from <i>Festuca arundinacea</i> . It contains a typical signature of the glycosyl hydrolases family 32 (amino acid residues 120 to 133). The glycosyl hydrolases family 32 domain signature has a consensus of HYQPxxH/NxxNDPNG, where D is the active site residue (Henrissat, <i>Biochem. J.</i> 280:309-316, 1991).
3 and 126	65 and 164	Fructan biosynthesis	Homolog of Sucrose:fructan 6-fructosyl-transferase (6-SFT) isolated from <i>Festuca arundinacea</i> . They contain a typical signature of the glycosyl hydrolases family 32 (amino acid residues 90 to 564). The glycosyl hydrolases family 32 domain signature has a consensus of HYQPxxH/NxxNDPNG, where D is the active site residue (Henrissat, <i>Biochem. J.</i> 280:309-316, 1991).
4 and 127	66 and 165	Fructan biosynthesis	Homolog of Sucrose:fructan 6-fructosyl-transferase (6-SFT) isolated from <i>Lolium perenne</i> . They contain a typical signature of the glycosyl hydrolases family 32 (amino acid residues 96 to 107). The glycosyl hydrolases family 32 domain signature has a consensus of HYQPxxH/NxxNDPNG, where D is the active site residue (Henrissat, <i>Biochem. J.</i> 280:309-316, 1991).
5	67	Fructan biosynthesis	Homolog of sucrose:fructan 6-fructosyl-transferase (6-SFT) isolated from <i>Festuca arundinacea</i> .
6 and 128	68 and 166	Fructan biosynthesis	Homolog of Sucrose:fructan 6-fructosyl-transferase (6-SFT) isolated from <i>Lolium perenne</i> . They contain a typical signature of the glycosyl hydrolases family 32 (amino acid

SEQ ID NO Polynucleotide	SEQ ID NO Polypeptide	Category	Description
			residues 90 to 103). The glycosyl hydrolases family 32 domain signature has a consensus of HYQPxxH/NxxNDPNG, where D is the active site residue (Henrissat, <i>Biochem. J.</i> 280:309-316, 1991).
7 and 129	69	Fructan biosynthesis	Homolog of Sucrose-6-phosphate phosphohydrolase (SPP; EC 3.1.3.24) isolated from <i>Festuca arundinacea</i> . This enzyme belongs to the superfamily of hydrolases, and has the three conserved motifs found in these proteins (Galperin and Koonin, <i>Trends Biochem Sci.</i> 23:127-129, 1998). Motif I (amino acid residues 10 to 19) contains conserved Asp and a Thr residues, motif II (amino acid residues 48 to 53) contains a conserved Thr residue, and Motif III (residues 167 to 220) contains conserved Lys (position 167) and Asp residues (position 202 and 206). These conserved amino acid residues are required for activity of the enzyme.
8	70	Fructan biosynthesis	Homolog of Sucrose-6-phosphate phosphohydrolase (SPP; EC 3.1.3.24) isolated from <i>Lolium perenne</i> . This enzyme belongs to the superfamily of hydrolases, and has the three conserved motifs found in these proteins (Galperin and Koonin, <i>Trends Biochem Sci.</i> 23:127-129, 1998). Motif I (residues 10 to 19) contains conserved Asp and Thr residues, motif II (amino acid residues 48 to 53) contains a conserved Thr residue, and Motif III (amino acid residues 167 to 220) contains conserved Lys (position 167) and Asp residues (position 202 and 206). These conserved amino acid residues are required for activity of the enzyme.
9 and 130	71	Fructan biosynthesis	Homolog of sucrose phosphate synthase (SPS-1) isolated from <i>Festuca arundinacea</i> .
10 and 131	72 and 167	Fructan biosynthesis	Homolog of sucrose phosphate synthase (SPS-1) isolated from <i>Lolium perenne</i> and that is involved in the sucrose synthesis pathway.
11 and 132	73 and 168	Fructan biosynthesis	Homolog of sucrose phosphate synthase (SPS-N) isolated from <i>Lolium perenne</i> and that is involved in the sucrose synthesis pathway.
12 and 133	74 and 169	Fructan	Homolog of sucrose synthase (SuS) isolated

SEQ ID NO Polynucleotide	SEQ ID NO Polypeptide	Category	Description
		biosynthesis	from <i>Lolium perenne</i> . These molecules contain a leucine zipper motif in amino acid position 191 to 213. Leucine zipper motifs are present in many gene regulatory proteins (Landschulz <i>et al.</i> , <i>Science</i> 240:1759-1764, 1988).
13	75	Fructan biosynthesis	Homolog of sucrose synthase (SuS) isolated from <i>Festuca arundinacea</i> . This molecule contains a leucine zipper motif in amino acid position 191 to 213. Leucine zipper motifs are present in many gene regulatory proteins (Landschulz <i>et al.</i> , <i>Science</i> 240:1759-1764, 1988).
14 and 134	76 and 170	Fructan biosynthesis	Homolog of sucrose synthase (SuS) isolated from <i>Lolium perenne</i> .
15	77	Fructan biosynthesis	Homolog of sucrose synthase (SuS) isolated from <i>Festuca arundinacea</i> .
16 and 135	78 and 171	Fructan biosynthesis	Homologue of cell wall invertase (CWINV) isolated from <i>Festuca arundinacea</i> that belongs to the family 32 of glycosyl hydrolases. These molecules contain a conserved peptide domain in amino acid residues 139 to 144 and 242-247, respectively. The consensus peptide domain of invertases is (WVYL)EC(PIL)D (LFI) with the conserved Cys residue part of the catalytic domain (Sturm, <i>Plant Physiol.</i> 121:1-7, 1999).
17	79	Fructan biosynthesis	Homolog of cell wall invertase (CWINV) isolated from <i>Lolium perenne</i> that belongs to the family 32 of glycosyl hydrolases. This molecule contains a conserved pentapeptide bF-motif at amino acid residues 70 to 74 and a peptide domain in amino acid residues 250 to 255. The consensus peptide domain of invertases is (WVYL)EC(PIL)D(LFI) with the conserved Cys residue part of the catalytic domain (Sturm, <i>Plant Physiol.</i> 121:1-7, 1999). It also contains a glycosyl hydrolases family 32 signature region at amino acids 61 to 74 that contains a conserved His residue important in the catalytic reaction (Reddy and Maley, <i>J. Biol. Chem.</i> 265:10817-10120, 1990).
18 and 136	80 and 172	Fructan biosynthesis	Homolog of cell wall invertase (CWINV) isolated from <i>Lolium perenne</i> that belongs to the family 32 of glycosyl hydrolases.
19	81	Fructan	Homolog of cell wall invertase (CWINV)

SEQ ID NO Polynucleotide	SEQ ID NO Polypeptide	Category	Description
		biosynthesis	isolated from <i>Festuca arundinacea</i> that belongs to the family 32 of glycosyl hydrolases. This molecule contains a conserved pentapeptide bF-motif at amino acid residues 60 to 64. The consensus peptide domain of invertases is (WVYL)EC(PIL)D(LFI) with the conserved Cys residue part of the catalytic domain (Sturm, <i>Plant Physiol.</i> 121:1-7, 1999). It also contains a glycosyl hydrolases family 32 signature region at amino acids 51 to 64 that contains a conserved His residue important in the catalytic reaction (Reddy and Maley, <i>J. Biol. Chem.</i> 265:10817-10120, 1990). A signal peptide is present in amino acid residues 1 to 24.
20 and 137	82 and 173	Fructan biosynthesis	Homolog of cell wall invertase (CWINV) isolated from <i>Festuca arundinacea</i> that belongs to the family 32 of glycosyl hydrolases. These molecules contain a peptide domain in amino acid residues 61 to 66 and 242-247, respectively. The consensus peptide domain of invertases is (WVYL)EC(PIL)D(LFI) with the conserved Cys residue part of the catalytic domain (Sturm, <i>Plant Physiol.</i> 121:1-7, 1999).
21	83	Fructan biosynthesis	Homolog of cell wall invertase (CWINV) isolated from <i>Festuca arundinacea</i> that belongs to the family 32 of glycosyl hydrolases. This molecule contains a conserved pentapeptide bF-motif at amino acid residues 73 to 77 and a peptide domain in amino acid residues 253 to 258. The consensus peptide domain of invertases is (WVYL)EC(PIL)D(LFI) with the conserved Cys residue part of the catalytic domain (Sturm, <i>Plant Physiol.</i> 121:1-7, 1999). It also contains a glycosyl hydrolases family 32 signature region at amino acid 64 to 77 that contains a conserved His residue important in the catalytic reaction (Reddy and Maley, <i>J. Biol. Chem.</i> 265:10817-10120, 1990).
22 and 138	84 and 174	Fructan biosynthesis	Homolog of cell wall invertase (CWINV) isolated from <i>Lolium perenne</i> that belongs to the family 32 of glycosyl hydrolases. These molecules contain a peptide domain in amino acid residues 174 to 179 and 234 to 239,

SEQ ID NO Polynucleotide	SEQ ID NO Polypeptide	Category	Description
			respectively. The consensus peptide domain of invertases is (WVYL)EC- (PIL)D(LFI) with the conserved Cys residue part of the catalytic domain (Sturm, <i>Plant Physiol.</i> 121:1-7, 1999).
23	85	Fructan biosynthesis	Homolog of cell wall invertase (CWINV) isolated from <i>Festuca arundinacea</i> that belongs to the family 32 of glycosyl hydrolases. This molecule contains a conserved pentapeptide bF-motif at amino acid residues 56 to 60. The consensus peptide domain of invertases is (WVYL)EC(PIL)D(LFI) with the conserved Cys residue part of the catalytic domain (Sturm, <i>Plant Physiol.</i> 121:1-7, 1999). It also contains a glycosyl hydrolases family 32 signature region at amino acid 47 to 60 that contains a conserved His residue that is important in the catalytic reaction (Reddy and Maley, <i>J. Biol. Chem.</i> 265:10817-10120, 1990). A signal peptide is present in amino acid residues 1 to 22.
24 and 139	86 and 175	Fructan biosynthesis	Homolog of cell wall invertase (CWINV) isolated from <i>Lolium perenne</i> that belongs to the family 32 of glycosyl hydrolases. These molecules contain a conserved pentapeptide bF-motif at amino acid residues 244 to 249. The consensus peptide domain of invertases is (WVYL)EC(PIL)D(LFI) with the conserved Cys residue part of the catalytic domain (Sturm, <i>Plant Physiol.</i> 121:1-7, 1999). They also contain a glycosyl hydrolases family 32 signature region at amino acid 56 to 69 that contains a conserved His residue that is important in the catalytic reaction (Reddy and Maley, <i>J. Biol. Chem.</i> 265:10817-10120, 1990). A signal peptide is present in amino acid residues 1 to 25.
25 and 140	87 and 176	Fructan biosynthesis	Homolog of vacuolar invertase (SINV) isolated from <i>Lolium perenne</i> that belongs to the family 32 of glycosyl hydrolases. These molecules contain a conserved pentapeptide bF-motif at amino acid residues 136 to 140 and 138 to 142, respectively and a peptide domain in amino acid residues 317 to 322 and 319 to 324, respectively. The consensus peptide domain of

SEQ ID NO Polynucleotide	SEQ ID NO Polypeptide	Category	Description
			invertases is (WVYL)EC(PIL)D(LFI) with the conserved Cys residue part of the catalytic domain (Sturm, <i>Plant Physiol.</i> 121:1-7, 1999). It also contains a glycosyl hydrolases family 32 signature region at amino acid 127 to 140 and 129 to 142 that contains a conserved His residue that is important in the catalytic reaction (Reddy and Maley, <i>J. Biol. Chem.</i> 265:10817-10120, 1990).
26 and 141	88 and 177	Fructan biosynthesis	Homolog of invertase (SINV) isolated from <i>Lolium perenne</i> that belongs to the family 32 of glycosyl hydrolases. These molecules contain a peptide domain in amino acid residues 143 to 148 and 184 to 189, respectively. The consensus peptide domain of invertases is (WVYL)EC(PIL)D(LFI) with the conserved Cys residue part of the catalytic domain (Sturm, <i>Plant Physiol.</i> 121:1-7, 1999).
27	89	Lignin/Tannin biosynthesis	Homolog of 4-Coumarate:CoA ligase (4CL, EC 6.2.1.12) isolated from <i>Lolium perenne</i> . The molecule has two conserved AMP binding regions at amino acid residues 182 to 193 and 383 to 389 (Hu <i>et al.</i> , <i>Proc. Natl. Acad. Sci. USA</i> 95:5407-5412, 1998). The AMP-binding domain signature consists of two binding site motifs. The consensus of the first motif is LPYSSGTTGLPK (Etchegaray <i>et al.</i> , <i>Biochem. Mol. Biol. Int.</i> 44:235-243, 1998). The region very rich in glycine, serine, and threonine followed by a conserved lysine. In most of these proteins, the residue that follows the Lys at the end of the pattern is a Gly. The second motif consensus sequence is GEIC(V/I)RG (Hu <i>et al.</i> , <i>Proc. Natl. Acad. Sci. USA</i> 95:5407-5412, 1998).
28 and 142	90	Lignin/Tannin biosynthesis	Homolog of 4-Coumarate:CoA ligase (4CL, EC 6.2.1.12) isolated from <i>Lolium perenne</i> . The molecule has two conserved AMP binding regions at amino acid residues 195 to 206 and 395 to 401 (Hu <i>et al.</i> , <i>Proc. Natl. Acad. Sci. USA</i> 95:5407-5412, 1998). The AMP-binding domain signature consists of two binding site motifs. The consensus of the first motif is LPYSSGTTGLPK (Etchegaray <i>et al.</i> ,

SEQ ID NO Polynucleotide	SEQ ID NO Polypeptide	Category	Description
			<i>Biochem. Mol. Biol. Int.</i> 44:235-243, 1998). The region very rich in glycine, serine, and threonine followed by a conserved lysine. In most of these proteins, the residue that follows the Lys at the end of the pattern is a Gly. The second motif consensus sequence is GEIC(V/I)RG (Hu <i>et al.</i> , <i>Proc. Natl. Acad. Sci. USA</i> 95:5407-5412, 1998).
29	91	Lignin/Tannin biosynthesis	Homolog of 4-Coumarate:CoA ligase (4CL, EC 6.2.1.12) isolated from <i>Festuca arundinacea</i> . The molecule has two conserved AMP binding regions at amino acid residues 195 to 206 and 395 to 401 (Hu <i>et al.</i> , <i>Proc. Natl. Acad. Sci. USA</i> 95:5407-5412, 1998). The AMP-binding domain signature consists of two binding site motifs. The consensus of the first motif is LPYSSGTTGLPK (Etchegaray <i>et al.</i> , <i>Biochem. Mol. Biol. Int.</i> 44:235-243, 1998). The region very rich in glycine, serine, and threonine followed by a conserved lysine. In most of these proteins, the residue that follows the Lys at the end of the pattern is a Gly. The second motif consensus sequence is GEIC(V/I)RG (Hu <i>et al.</i> , <i>Proc. Natl. Acad. Sci. USA</i> 95:5407-5412, 1998).
30 and 143	92 and 178	Lignin/Tannin biosynthesis	Homolog of 4-Coumarate:CoA ligase (4CL, EC 6.2.1.12) isolated from <i>Lolium</i> . The molecules have two conserved AMP binding regions at amino acid residues 194 to 205 and 394 to 400 (Hu <i>et al.</i> , <i>Proc. Natl. Acad. Sci. USA</i> 95:5407-5412, 1998). The AMP-binding domain signature consists of two binding site motifs. The consensus of the first motif is LPYSSGTTGLPK (Etchegaray <i>et al.</i> , <i>Biochem. Mol. Biol. Int.</i> 44:235-243, 1998). The region very rich in glycine, serine, and threonine followed by a conserved lysine. In most of these proteins, the residue that follows the Lys at the end of the pattern is a Gly. The second motif consensus sequence is GEIC(V/I)RG (Hu <i>et al.</i> , <i>Proc. Natl. Acad. Sci. USA</i> 95:5407-5412, 1998).
31	93	Lignin/Tannin biosynthesis	Homolog of 4-Coumarate:CoA ligase (4CL, EC 6.2.1.12) isolated from <i>Festuca</i>

SEQ ID NO Polynucleotide	SEQ ID NO Polypeptide	Category	Description
			<i>arundinacea</i> . The molecule has two conserved AMP binding regions at amino acid residues 194 to 206 and 482 to 490 (Hu <i>et al.</i> , <i>Proc. Natl. Acad. Sci. USA</i> 95:5407-5412, 1998). The AMP-binding domain signature consists of two binding site motifs. The consensus of the first motif is LPYSSGTTGLPK (Etchegaray <i>et al.</i> , <i>Biochem. Mol. Biol. Int.</i> 44:235-243, 1998). The region very rich in glycine, serine, and threonine followed by a conserved lysine. In most of these proteins, the residue that follows the Lys at the end of the pattern is a Gly. The second motif consensus sequence is GEIC(V/I)RG (Hu <i>et al.</i> , <i>Proc. Natl. Acad. Sci. USA</i> 95:5407-5412, 1998).
32 and 144	94 and 179	Lignin/Tannin biosynthesis	Homolog of cinnamic acid 4-hydroxylase (C4H) isolated from <i>Lolium perenne</i> . The molecules have a conserved cytochrome P450 region in amino acids 436 to 445 that contains a conserved Cys residue involved in heme binding (Miles <i>et al.</i> , <i>Biochim Biophys Acta</i> 1543:383-407, 2000).
33	95	Lignin/Tannin biosynthesis	Homolog of cinnamic acid 4-hydroxylase (C4H) isolated from <i>Festuca arundinacea</i> . The molecule has a conserved Cytochrome P450 region in amino acids 440 to 449 that contains a conserved Cys residue involved in heme binding. The cytochrome P450 cysteine heme-iron ligand signature consensus is FGxGRRSCPG where the conserved C is the heme iron ligand (Miles <i>et al.</i> , <i>Biochim. Biophys. Acta</i> 1543:383-407, 2000). It also contains an aldehyde dehydrogenases active site (Hempel <i>et al.</i> , <i>Adv. Exp. Med. Biol.</i> 436:53-59, 1999) at amino acid residues 428 to 435. A hydrophobic signal peptide region is present in amino acid residues 1 to 24.
34 and 145	96 and 180	Lignin biosynthesis	Homolog of cinnamyl-alcohol dehydrogenase (CAD; EC 1.1.1.195) isolated from <i>Lolium perenne</i> . These molecules contain a conserved zinc-containing alcohol dehydrogenase domain (Joernvall <i>et al.</i> , <i>Eur. J. Biochem.</i> 167:195-201, 1987) in amino acid residues 69 to 83, with a conserved His residue at position 70. They also

SEQ ID NO Polynucleotide	SEQ ID NO Polypeptide	Category	Description
			contain a cytochrome C family heme-binding site signature (Mathews, <i>Prog. Biophys. Mol. Biol.</i> 45:1-56, 1985) in residues 45 to 50.
35	97	Lignin biosynthesis	Homolog of cinnamyl-alcohol dehydrogenase (CAD; EC 1.1.1.195) isolated from <i>Festuca arundinacea</i> . CAD belongs to the family of zinc-binding dehydrogenases. This molecule contains a conserved zinc-containing alcohol dehydrogenases domain (Joernvall <i>et al.</i> , <i>Eur. J. Biochem.</i> 167:195-201, 1987) in amino acid residues 69 to 83, with a conserved His residue at position 70. It also contains a Cytochrome C family heme-binding site signature. The cytochrome C family heme-binding site signature is CGICHT. In the cytochrome C protein family, the heme group is covalently attached by thioether bonds to two conserved cysteine residues. The consensus sequence for this site is Cys-X-X-Cys-His and the histidine residue is one of the two axial ligands of the heme iron. This arrangement is shared by all proteins known to belong to cytochrome C family (Mathews, <i>Prog. Biophys. Mol. Biol.</i> 45:1-56, 1985).
36 and 146	98	Lignin biosynthesis	Homolog of caffeoyl coenzyme A O-methyltransferase (CCoAOMT) (EC 2.1.1.104) isolated from <i>Lolium perenne</i> .
37	99	Lignin biosynthesis	Homolog of caffeoyl coenzyme A O-methyltransferase (CCoAOMT) (EC 2.1.1.104) isolated from <i>Festuca arundinacea</i> .
38 and 147	100 and 181	Lignin biosynthesis	Homolog of cinnamoyl CoA:NADP oxidoreductase (CCR, EC 1.2.1.44) isolated from <i>Lolium perenne</i> that catalyzes the conversion of cinnamoyl CoA esters to their corresponding cinnamaldehydes in the first specific step in the synthesis of the lignin monomers. A hydrophobic region typical of a signal peptide is present in amino acid residues 1 to 24.
39 and 148	101	Lignin biosynthesis	Homolog of cinnamoyl CoA:NADP oxidoreductase (CCR, EC 1.2.1.44) isolated from <i>Festuca arundinacea</i> that catalyzes the conversion of cinnamoyl CoA esters to their corresponding cinnamaldehydes in the first

SEQ ID NO Polynucleotide	SEQ ID NO Polypeptide	Category	Description
			specific step in the synthesis of the lignin monomers.
40 and 149	102 and 182	Lignin biosynthesis	Homolog of caffeic acid 3-O-methyltransferase (COMT1) isolated from <i>Festuca arundinacea</i> . A conserved consensus phosphopantetheine attachment site was identified in amino acid residues 47 to 62. This domain is involved in the attachment of activated fatty acid and amino-acid groups, with the Ser residue at position 52 crucial for the phosphopantetheine attachment (Pugh and Wakil, <i>J. Biol. Chem.</i> 240:4727-4733, 1965).
41 and 150	103	Lignin biosynthesis	Homolog of caffeic acid 3-O-methyltransferase (COMT1) isolated from <i>Lolium perenne</i> . A conserved consensus phosphopantetheine attachment site was identified in amino acid residues 47 to 62. This domain is involved in the attachment of activated fatty acid and amino-acid groups, with the Ser residue at position 52 crucial for the phosphopantetheine attachment (Pugh and Wakil, <i>J. Biol. Chem.</i> 240:4727-4733, 1965).
42	104	Lignin biosynthesis	Homolog of caffeic acid 3-O-methyltransferase (COMT1) isolated from <i>Festuca arundinacea</i> . A conserved consensus phosphopantetheine attachment site was identified in amino acid residues 47 to 62. This domain is involved in the attachment of activated fatty acid and amino-acid groups, with the Ser residue at position 52 crucial for the phosphopantetheine attachment (Pugh and Wakil, <i>J. Biol. Chem.</i> 240:4727-4733, 1965).
43	105	Lignin biosynthesis	Homolog of caffeic acid 3-O-methyltransferase (COMT1) isolated from <i>Lolium perenne</i> . A conserved consensus phosphopantetheine attachment site was identified in amino acid residues 47 to 62. This domain is involved in the attachment of activated fatty acid and amino-acid groups, with the Ser residue at position 52 crucial for the phosphopantetheine attachment (Pugh and Wakil, <i>J. Biol. Chem.</i> 240:4727-4733, 1965).
44 and 151	106 and 183	Lignin biosynthesis	Homolog of ferulate 5-hydroxylase (F5H) isolated from <i>Lolium perenne</i> . The molecules

SEQ ID NO Polynucleotide	SEQ ID NO Polypeptide	Category	Description
			have a conserved cytochrome P450 region in amino acids 463 to 472 that contains a conserved Cys residue involved in heme binding (Miles <i>et al.</i> , <i>Biochim Biophys Acta</i> 1543:383-407, 2000). A signal peptide is present in amino acid residues 1 to 30.
45	107	Lignin biosynthesis	Homolog of ferulate 5-hydroxylase (F5H) isolated from <i>Festuca arundinaceae</i> . The molecule has a conserved cytochrome P450 region in amino acids 462 to 471 that contains a conserved Cys residue involved in heme binding (Miles <i>et al.</i> , <i>Biochim Biophys Acta</i> 1543:383-407, 2000). A signal peptide is present in amino acid residues 1 to 30.
46 and 152	108	Lignin/Tannin biosynthesis	Homolog of phenylalanine ammonia-lyase (EC 4.3.1.5) (PAL) isolated from <i>Lolium perenne</i> . The polypeptide has a conserved PAL-histidase region in amino acid residues 193 to 209.
47 and 153	109 and 184	Lignin/Tannin biosynthesis	Homolog of phenylalanine ammonia-lyase (EC 4.3.1.5) (PAL) isolated from <i>Festuca arundinacea</i> . A conserved phenylalanine and histidine ammonia-lyases active site signature has been identified in amino acid residues 195 to 210.
48	110	Lignin biosynthesis	Homolog of peroxidase (PER) isolated from <i>Festuca arundinacea</i> . The conserved peroxidase I region is present in amino acid residues 188 to 199 and contains a conserved His residue at position 196 in the active site, and the conserved peroxidase 2 region is present in amino acid residues 60 to 71, with a conserved His residue at position 69 that is involved in heme binding (Kimura and Ikeda-Saito, <i>Proteins</i> 3:113-120, 1988). A signal peptide is present in amino acid residues 1 to 27.
49	111	Lignin biosynthesis	Homolog of peroxidase (PER) isolated from <i>Lolium perenne</i> . The conserved peroxidase I region is present in amino acid residues 199 to 209 and contains a conserved His residue at position 208 in the active site. A signal peptide is present in amino acid residues 1 to 33.
50	112	Lignin biosynthesis	Homolog of peroxidase (PER) isolated from <i>Festuca arundinacea</i> . The conserved

SEQ ID NO Polynucleotide	SEQ ID NO Polypeptide	Category	Description
			peroxidase I region is present in amino acid residues 180 to 190 and contains a conserved His residue at position 188 in the active site, and the conserved peroxidase 2 region is present in amino acid residues 55 to 66, with a conserved His residue at position 64 that is involved in heme binding (Kimura and Ikeda-Saito, <i>Proteins</i> 3:113-120, 1988). A signal peptide is present in amino acid residues 1 to 22.
51 and 154	113	Lignin biosynthesis	Homolog of peroxidase (PER) isolated from <i>Lolium perenne</i> . The conserved peroxidase I region is present in amino acid residues 199 to 209 and contains a conserved His residue at position 207 in the active site, and the conserved peroxidase 2 region is present in amino acid residues 70 to 80, with a conserved His residue at position 78 that is involved in heme binding (Kimura and Ikeda-Saito, <i>Proteins</i> 3:113-120, 1988). A signal peptide is present in amino acid residues 1 to 20.
52 and 155	114	Lignin biosynthesis	Homolog of peroxidase (PER) isolated from <i>Lolium perenne</i> . The conserved peroxidase I region is present in amino acid residues 198 to 208 and contains a conserved His residue at position 206 in the active site (Kimura and Ikeda-Saito, <i>Proteins</i> 3:113-120, 1988). A signal peptide is present in amino acid residues 1 to 34.
53, 156, and 162	115, 185, and 190	Lignin biosynthesis	Homolog of peroxidase (PER) isolated from <i>Lolium perenne</i> . The conserved peroxidase I region is present in amino acid residues 157 to 168, 188 to 199, and 190 to 201, respectively and contain a conserved His residue at position 165, 196 and 198, respectively in the active site, and the conserved peroxidase 2 region is present in amino acid residues 29 to 41, 60 to 72 and 62 to 74, respectively, with a conserved His residue at position 38, 69 and 71, respectively that is involved in heme binding (Kimura and Ikeda-Saito, <i>Proteins</i> 3:113-120, 1988).
54	116	Lignin biosynthesis	Homolog of peroxidase (PER) isolated from <i>Festuca arundinacea</i> . The conserved

SEQ ID NO Polynucleotide	SEQ ID NO Polypeptide	Category	Description
			peroxidase I region is present in amino acid residues 176 to 186 and contains a conserved His residue at position 184 in the active site, and the conserved peroxidase 2 region is present in amino acid residues 55 to 67, with a conserved His residue at position 64 that is involved in heme binding (Kimura and Ikeda-Saito, <i>Proteins</i> 3:113-120, 1988). A signal peptide is present in amino acid residues 1 to 22.
55	117	Tannin Biosynthesis	Homolog of chalcone isomerase (CHI) isolated from <i>Lolium perenne</i> . The molecule contains a chalcone isomerase region at amino acid residues 1 to 213.
56	118	Tannin Biosynthesis	Homolog of chalcone isomerase (CHI). The molecule contains a chalcone isomerase region at amino acid residues 23 to 235.
57 and 157	119 and 186	Tannin Biosynthesis	Homolog of Chalcone Synthase (CHS) isolated from <i>Lolium perenne</i> and that is an important enzyme in flavonoid synthesis. The molecules contain a conserved chalcone synthase active site (Lanz <i>et al.</i> , <i>J. Biol. Chem.</i> 266:9971-9976, 1991) at amino acid residues 166 to 175, with the conserved Cys residue at position 167.
58 and 158	120 and 187	Tannin Biosynthesis	Homolog of dihydroflavonal-4-reductase (DFR) isolated from <i>Festuca arundinacea</i> .
59 and 159	121 and 188	Tannin Biosynthesis	Homolog of dihydroflavonal-4-reductase (DFR) isolated from <i>Lolium perenne</i> .
60 and 160	122 and 189	Tannin Biosynthesis	Homolog of dihydroflavonal-4-reductase (DFR) isolated from <i>Lolium perenne</i> . These molecules contain a conserved ATP/GTP binding site at amino acid residues 84 to 91 and 86 to 93, respectively, known as the "A" sequence (Walker <i>et al.</i> , <i>EMBO J.</i> 1:945-951, 1982) or "P-loop" (Saraste <i>et al.</i> , <i>Trends Biochem. Sci.</i> 15:430-434, 1990).
61 and 161	123	Tannin biosynthesis	Homolog of flavanone 3- β hydroxylase (F3 β H) isolated from <i>Lolium perenne</i> .
62	124	Tannin Biosynthesis	Homolog of flavanone 3- β hydroxylase (F3 β H) isolated from <i>Festuca arundinacea</i> .

All the polynucleotides and polypeptides provided by the present invention are isolated and purified, as those terms are commonly used in the art. Preferably, the polypeptides and polynucleotides are at least about 80% pure, more preferably at least about 90% pure, and most preferably at least about 99% pure.

5 The word "polynucleotide(s)," as used herein, means a polymeric collection of nucleotides, and includes DNA and corresponding RNA molecules and both single and double stranded molecules, including RNAi, HnRNA and mRNA molecules, sense and anti-sense strands of DNA and RNA molecules, and comprehends cDNA, genomic DNA, and wholly or partially synthesized polynucleotides. A polynucleotide of the present invention
10 may be an entire gene, or any portion thereof. As used herein, a "gene" is a DNA sequence which codes for a functional protein or RNA molecule. Operable anti-sense polynucleotides may comprise a fragment of the corresponding polynucleotide, and the definition of "polynucleotide" therefore includes all operable anti-sense fragments. Anti-sense polynucleotides and techniques involving anti-sense polynucleotides are well known in the
15 art and are described, for example, in Robinson-Benion *et al.*, *Methods in Enzymol.* 254(23): 363-375, 1995 and Kawasaki *et al.*, *Artific. Organs* 20(8): 836-848, 1996.

In specific embodiments, the present invention provides isolated polynucleotides comprising a sequence of SEQ ID NO: 1-62 and 125-162; polynucleotides comprising variants of SEQ ID NO: 1-62 and 125-162; polynucleotides comprising extended sequences
20 of SEQ ID NO: 1-62 and 125-162 and their variants, oligonucleotide primers and probes corresponding to the sequences set out in SEQ ID NO: 1-62 and 125-162 and their variants, polynucleotides comprising at least a specified number of contiguous residues of any of SEQ ID NO: 1-62 and 125-162 (*x*-mers), and polynucleotides comprising extended sequences which include portions of the sequences set out in SEQ ID NO: 1-62 and 125-162, all of
25 which are referred to herein, collectively, as "polynucleotides of the present invention." Polynucleotides that comprise complements of such polynucleotide sequences, reverse complements of such polynucleotide sequences, or reverse sequences of such polynucleotide sequences, together with variants of such sequences, are also provided.

The definition of the terms "complement(s)," "reverse complement(s)," and "reverse
30 sequence(s)," as used herein, is best illustrated by the following example. For the sequence 5' AGGACC 3', the complement, reverse complement, and reverse sequence are as follows:

complement	3' TCCTGG 5'
reverse complement	3' GGTCCT 5'
reverse sequence	5' CCAGGA 3'.

Preferably, sequences that are complements of a specifically recited polynucleotide
 5 sequence are complementary over the entire length of the specific polynucleotide sequence.

As used herein, the term "x-mer," with reference to a specific value of "x," refers to a polynucleotide comprising at least a specified number ("x") of contiguous residues of: any of the polynucleotides provided in SEQ ID NO: 1-62 and 125-162. The value of x may be from about 20 to about 600, depending upon the specific sequence.

10 Polynucleotides of the present invention comprehend polynucleotides comprising at least a specified number of contiguous residues (x-mers) of any of the polynucleotides identified as SEQ ID NO: 1-62 and 125-162, or their variants. Similarly, polypeptides of the present invention comprehend polypeptides comprising at least a specified number of contiguous residues (x-mers) of any of the polypeptides identified as SEQ ID NO: 63-124
 15 and 163-190. According to preferred embodiments, the value of x is at least 20, more preferably at least 40, more preferably yet at least 60, and most preferably at least 80. Thus, polynucleotides of the present invention include polynucleotides comprising a 20-mer, a 40-mer, a 60-mer, an 80-mer, a 100-mer, a 120-mer, a 150-mer, a 180-mer, a 220-mer, a 250-mer; or a 300-mer, 400-mer, 500-mer or 600-mer of a polynucleotide provided in SEQ ID
 20 NO: 1-62 and 125-162, or a variant of one of the polynucleotides corresponding to the polynucleotides provided in SEQ ID NO: 1-62 and 125-162. Polypeptides of the present invention include polypeptides comprising a 20-mer, a 40-mer, a 60-mer, an 80-mer, a 100-mer, a 120-mer, a 150-mer, a 180-mer, a 220-mer, a 250-mer; or a 300-mer, 400-mer, 500-mer or 600-mer of a polypeptide provided in SEQ ID NO: 63-124 and 163-190, or a variant
 25 thereof.

Polynucleotides of the present invention were isolated by high throughput sequencing of cDNA libraries comprising forage grass tissue collected from *Lolium perenne* and *Festuca arundinacea*. Some of the polynucleotides of the present invention may be "partial" sequences, in that they do not represent a full-length gene encoding a full-length polypeptide.
 30 Such partial sequences may be extended by analyzing and sequencing various DNA libraries using primers and/or probes and well known hybridization and/or PCR techniques. Partial

sequences may be extended until an open reading frame encoding a polypeptide, a full-length polynucleotide and/or gene capable of expressing a polypeptide, or another useful portion of the genome is identified. Such extended sequences, including full-length polynucleotides and genes, are described as "corresponding to" a sequence identified as one of the sequences of SEQ ID NO: 1-62 and 125-162 or a variant thereof, or a portion of one of the sequences of SEQ ID NO: 1-62 and 125-162 or a variant thereof, when the extended polynucleotide comprises an identified sequence or its variant, or an identified contiguous portion (x-mer) of one of the sequences of SEQ ID NOS: 1-62 and 125-162 or a variant thereof. Similarly, RNA sequences, reverse sequences, complementary sequences, anti-sense sequences and the like, corresponding to the polynucleotides of the present invention, may be routinely ascertained and obtained using the cDNA sequences identified as SEQ ID NOS: 1-62 and 125-162.

The polynucleotides identified as SEQ ID NOS: 1-62 and 125-162 contain open reading frames ("ORFs") or partial open reading frames encoding polypeptides and functional portions of polypeptides. Additionally, open reading frames encoding polypeptides may be identified in extended or full length sequences corresponding to the sequences set out as SEQ ID NOS: 1-62 and 125-162. Open reading frames may be identified using techniques that are well known in the art. These techniques include, for example, analysis for the location of known start and stop codons, most likely reading frame identification based on codon frequencies, etc. These techniques include, for example, analysis for the location of known start and stop codons, most likely reading frame identification based on codon frequencies, etc. Suitable tools and software for ORF analysis are well known in the art and include, for example, GeneWise, available from The Sanger Center, Wellcome Trust Genome Campus, Hinxton, Cambridge, CB10 1SA, United Kingdom; Diogenes, available from Computational Biology Centers, University of Minnesota, Academic Health Center, UMHG Box 43 Minneapolis MN 55455; and GRAIL, available from the Informatics Group, Oak Ridge National Laboratories, Oak Ridge, Tennessee TN. Once a partial open reading frame is identified, the polynucleotide may be extended in the area of the partial open reading frame using techniques that are well known in the art until the polynucleotide for the full open reading frame is identified.

Once open reading frames are identified in the polynucleotides of the present invention, the open reading frames may be isolated and/or synthesized. Expressible genetic constructs comprising the open reading frames and suitable promoters, initiators, terminators, etc., which are well known in the art, may then be constructed. Such genetic constructs may
5 be introduced into a host cell to express the polypeptide encoded by the open reading frame. Suitable host cells may include various prokaryotic and eukaryotic cells, including plant cells, mammalian cells, bacterial cells, algae and the like.

The polynucleotides of the present invention may be isolated by high throughput sequencing of cDNA libraries prepared from forage grass tissue, as described below in
10 Example 1. Alternatively, oligonucleotide probes and primers based on the sequences provided in SEQ ID NOS: 1-62 and 125-162 can be synthesized as detailed below, and used to identify positive clones in either cDNA or genomic DNA libraries from forage grass tissue cells by means of hybridization or polymerase chain reaction (PCR) techniques. Hybridization and PCR techniques suitable for use with such oligonucleotide probes are well
15 known in the art (*see, for example, Mullis et al., Cold Spring Harbor Symp. Quant. Biol.*, 51:263, 1987; Erlich, ed., *PCR technology*, Stockton Press: NY, 1989; and Sambrook *et al.*, eds., *Molecular cloning: a laboratory manual*, 2nd ed., CSHL Press: Cold Spring Harbor, NY, 1989). In addition to DNA-DNA hybridization, DNA-RNA or RNA-RNA hybridization assays are also possible. In the first case, the mRNA from expressed genes would then be
20 detected instead of genomic DNA or cDNA derived from mRNA of the sample. In the second case, RNA probes could be used. Artificial analogs of DNA hybridizing specifically to target sequences could also be employed. Positive clones may be analyzed by restriction enzyme digestion, DNA sequencing or the like.

The polynucleotides of the present invention may also, or alternatively, be
25 synthesized using techniques that are well known in the art. The polynucleotides may be synthesized, for example, using automated oligonucleotide synthesizers (*e.g.*, Beckman Oligo 1000M DNA Synthesizer; Beckman Coulter Ltd., Fullerton, CA) to obtain polynucleotide segments of up to 50 or more nucleic acids. A plurality of such polynucleotide segments may then be ligated using standard DNA manipulation techniques that are well known in the
30 art of molecular biology. One conventional and exemplary polynucleotide synthesis technique involves synthesis of a single stranded polynucleotide segment having, for

example, 80 nucleic acids, and hybridizing that segment to a synthesized complementary 85 nucleic acid segment to produce a 5 nucleotide overhang. The next segment may then be synthesized in a similar fashion, with a 5 nucleotide overhang on the opposite strand. The “sticky” ends ensure proper ligation when the two portions are hybridized. In this way, a
5 complete polynucleotide of the present invention may be synthesized entirely *in vitro*.

Oligonucleotide probes and primers complementary to and/or corresponding to SEQ ID NOS: 1-62 and 125-162, and variants of those sequences, are also comprehended by the present invention. Such oligonucleotide probes and primers are substantially complementary to the polynucleotide of interest over a certain portion of the polynucleotide. An
10 oligonucleotide probe or primer is described as “corresponding to” a polynucleotide of the present invention, including one of the sequences set out as SEQ ID NOS: 1-62 and 125-162 or a variant thereof, if the oligonucleotide probe or primer, or its complement, is contained within one of the sequences set out as SEQ ID NOS: 1-62 and 125-162 or a variant of one of the specified sequences.

15 Two single stranded sequences are said to be substantially complementary when the nucleotides of one strand, optimally aligned and compared, with the appropriate nucleotide insertions and/or deletions, pair with at least 80%, preferably at least 90% to 95%, and more preferably at least 98% to 100%, of the nucleotides of the other strand. Alternatively, substantial complementarity exists when a first DNA strand will selectively hybridize to a
20 second DNA strand under stringent hybridization conditions.

In specific embodiments, the oligonucleotide probes and/or primers comprise at least about 6 contiguous residues, more preferably at least about 10 contiguous residues, and most preferably at least about 20 contiguous residues complementary to a polynucleotide sequence of the present invention. Probes and primers of the present invention may be from about 8 to
25 100 base pairs in length, preferably from about 10 to 50 base pairs in length, and more preferably from about 15 to 40 base pairs in length. The probes can be easily selected using procedures well known in the art, taking into account DNA-DNA hybridization stringencies, annealing and melting temperatures, potential for formation of loops, and other factors which are well known in the art. Preferred techniques for designing PCR primers are disclosed in
30 Dieffenbach and Dyksler, *PCR Primer: a laboratory manual*, CSHL Press: Cold Spring Harbor, NY, 1995. A software program suitable for designing probes, and especially for

designing PCR primers, is available from Premier Biosoft International, 3786 Corina Way, Palo Alto, CA 94303-4504.

The isolated polynucleotides of the present invention also have utility in genome mapping, in physical mapping, and in positional cloning of genes.

5 The polynucleotides identified as SEQ ID NOS: 1-62 and 125-162 were isolated from cDNA clones and represent sequences that are expressed in the tissue from which the cDNA was prepared. RNA sequences, reverse sequences, complementary sequences, anti-sense sequences, and the like, corresponding to the polynucleotides of the present invention, may be routinely ascertained and obtained using the cDNA sequences identified as SEQ ID
10 NOS: 1-62 and 125-162.

Identification of genomic DNA and heterologous species DNA can be accomplished by standard DNA/DNA hybridization techniques, under appropriately stringent conditions, using all or part of a polynucleotide sequence as a probe to screen an appropriate library. Alternatively, PCR techniques using oligonucleotide primers that are designed based on
15 known genomic DNA, cDNA and protein sequences can be used to amplify and identify genomic and cDNA sequences.

In another aspect, the present invention provides isolated polypeptides encoded by the above polynucleotides. As used herein, the term "polypeptide" encompasses amino acid chains of any length, including full-length proteins, wherein the amino acid residues are
20 linked by covalent peptide bonds. The term "polypeptide encoded by a polynucleotide" as used herein, includes polypeptides encoded by a polynucleotide that comprises a partial isolated polynucleotide sequence provided herein. In specific embodiments, the inventive polypeptides comprise an amino acid sequence selected from the group consisting of SEQ ID NO: 63-124 and 163-190, as well as variants of such sequences.

25 As noted above, polypeptides of the present invention may be produced recombinantly by inserting a polynucleotide sequence of the present invention encoding the polypeptide into an expression vector and expressing the polypeptide in an appropriate host. Any of a variety of expression vectors known to those of ordinary skill in the art may be employed. Expression may be achieved in any appropriate host cell that has been
30 transformed or transfected with an expression vector containing a polynucleotide molecule that encodes a recombinant polypeptide. Suitable host cells include prokaryotes, yeast, and

higher eukaryotic cells. Preferably, the host cells employed are plant, *E. coli*, insect, yeast, or a mammalian cell line such as COS or 293T. The polynucleotide sequences expressed in this manner may encode naturally occurring polypeptides, portions of naturally occurring polypeptides, or other variants thereof. The expressed polypeptides may be used in various assays known in the art to determine their biological activity. Such polypeptides may also be used to raise antibodies, to isolate corresponding interacting proteins or other compounds, and to quantitatively determine levels of interacting proteins or other compounds.

In a related aspect, polypeptides are provided that comprise at least a functional portion of a polypeptide having an amino acid sequence selected from the group consisting of sequences provided in SEQ ID NO: 63-124 and 163-190, and variants thereof. As used herein, the "functional portion" of a polypeptide is that portion which contains an active site essential for affecting the function of the polypeptide, for example, a portion of the molecule that is capable of binding one or more reactants. The active site may be made up of separate portions present on one or more polypeptide chains and will generally exhibit high binding affinity. Functional portions of a polypeptide may be identified by first preparing fragments of the polypeptide by either chemical or enzymatic digestion of the polypeptide, or by mutation analysis of the polynucleotide that encodes the polypeptide and subsequent expression of the resulting mutant polypeptides. The polypeptide fragments or mutant polypeptides are then tested to determine which portions retain biological activity, using methods well known to those of skill in the art, including the representative assays described below.

Portions and other variants of the inventive polypeptides may be generated by synthetic or recombinant means. Synthetic polypeptides having fewer than about 100 amino acids, and generally fewer than about 50 amino acids, may be generated using techniques well known to those of ordinary skill in the art. For example, such polypeptides may be synthesized using any of the commercially available solid-phase techniques, such as the Merrifield solid-phase synthesis method, where amino acids are sequentially added to a growing amino acid chain. See Merrifield, *J. Am. Chem. Soc.* 85:2149-2146, 1963. Equipment for automated synthesis of polypeptides is commercially available from suppliers such as Perkin Elmer/Applied Biosystems, Inc. (Foster City, California), and may be operated according to the manufacturer's instructions. Variants of a native polypeptide may

be prepared using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis (Kunkel, *Proc. Natl. Acad. Sci. USA* 82:488-492, 1985). Sections of DNA sequences may also be removed using standard techniques to permit preparation of truncated polypeptides.

5 As used herein, the term "variant" comprehends nucleotide or amino acid sequences different from the specifically identified sequences, wherein one or more nucleotides or amino acid residues is deleted, substituted, or added. Variants may be naturally occurring allelic variants, or non-naturally occurring variants. Variant sequences (polynucleotide or polypeptide) preferably exhibit at least 75%, more preferably at least 80%, more preferably
10 at least 90%, more preferably yet at least 95% and most preferably, at least 98% identity to a sequence of the present invention. The percentage identity is determined by aligning the two sequences to be compared as described below, determining the number of identical residues in the aligned portion, dividing that number by the total number of residues in the inventive (queried) sequence, and multiplying the result by 100.

15 Polynucleotides and polypeptides having a specified percentage identity to a polynucleotide or polypeptide identified in one of SEQ ID NO: 1-190 thus share a high degree of similarity in their primary structure. In addition to a specified percentage identity to a polynucleotide or polypeptide of the present invention, variant polynucleotides and polypeptides preferably have additional structural and/or functional features in common with
20 a polynucleotide of the present invention. Polynucleotides having a specified degree of identity to, or capable of hybridizing to, a polynucleotide of the present invention preferably additionally have at least one of the following features: (1) they contain an open reading frame, or partial open reading frame, encoding a polypeptide, or a functional portion of a polypeptide, having substantially the same functional properties as the polypeptide, or
25 functional portion thereof, encoded by a polynucleotide in a recited SEQ ID NO:; or (2) they contain identifiable domains in common. Similarly, polypeptides having a specified degree of identity to a polypeptide of the present invention preferably additionally have at least one of the following features: (1) they have substantially the same functional properties as the polypeptide in the recited SEQ ID NO:; or (2) they contain identifiable domains in common.

30 Polynucleotide or polypeptide sequences may be aligned, and percentages of identical nucleotides or amino acids in a specified region may be determined against another

polynucleotide or polypeptide, using computer algorithms that are publicly available. The BLASTN and FASTA algorithms, set to the default parameters described in the documentation and distributed with the algorithm, may be used for aligning and identifying the similarity of polynucleotide sequences. The alignment and similarity of polypeptide sequences may be examined using the BLASTP algorithm. BLASTX and FASTX algorithms compare nucleotide query sequences translated in all reading frames against polypeptide sequences. The FASTA and FASTX algorithms are described in Pearson and Lipman, *Proc. Natl. Acad. Sci. USA* 85:2444-2448, 1988; and in Pearson, *Methods in Enzymol.* 183:63-98, 1990. The FASTA software package is available from the University of Virginia by contacting the Assistant Provost for Research, University of Virginia, PO Box 9025, Charlottesville, VA 22906-9025. The BLASTN software is available from the National Center for Biotechnology Information (NCBI), National Library of Medicine, Building 38A, Room 8N805, Bethesda, MD 20894. The BLASTN algorithm Version 2.0.11 [Jan-20-2000] and Version 2.2.1 [Apr-13-2001] set to the default parameters described in the documentation and distributed with the algorithm, are preferred for use in the determination of polynucleotide variants according to the present invention. The use of the BLAST family of algorithms, including BLASTN, BLASTP and BLASTX, is described in the publication of Altschul *et al.*, "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs," *Nucleic Acids Res.* 25:3389-3402, 1997.

The following running parameters are preferred for determination of alignments and similarities using BLASTN that contribute to the E values and percentage identity for polynucleotides: Unix running command with the following default parameters: blastall -p blastn -d embldb -e 10 -G 0 -E 0 -r 1 -v 30 -b 30 -i queryseq -o results; and parameters are: -p Program Name [String]; -d Database [String]; -e Expectation value (E) [Real]; -G Cost to open a gap (zero invokes default behavior) [Integer]; -E Cost to extend a gap (zero invokes default behavior) [Integer]; -r Reward for a nucleotide match (BLASTN only) [Integer]; -v Number of one-line descriptions (V) [Integer]; -b Number of alignments to show (B) [Integer]; -i Query File [File In]; -o BLAST report Output File [File Out] Optional.

The following running parameters are preferred for determination of alignments and similarities using BLASTP that contribute to the E values and percentage identity of

polypeptide sequences: blastall -p blastp -d swissprot db -e 10 -G 0 -E 0 -v 30 -b 30 -i queryseq -o results; the parameters are: -p Program Name [String]; -d Database [String]; -e Expectation value (E) [Real]; -G Cost to open a gap (zero invokes default behavior) [Integer]; -E Cost to extend a gap (zero invokes default behavior) [Integer]; -v Number of
 5 one-line descriptions (v) [Integer]; -b Number of alignments to show (b) [Integer]; -I Query File [File In]; -o BLAST report Output File [File Out] Optional.

The "hits" to one or more database sequences by a queried sequence produced by BLASTN, BLASTP, FASTA, or a similar algorithm, align and identify similar portions of sequences. The hits are arranged in order of the degree of similarity and the length of
 10 sequence overlap. Hits to a database sequence generally represent an overlap over only a fraction of the sequence length of the queried sequence.

As noted above, the percentage identity of a polynucleotide or polypeptide sequence is determined by aligning polynucleotide and polypeptide sequences using appropriate algorithms, such as BLASTN or BLASTP, respectively, set to default parameters; identifying
 15 the number of identical nucleic or amino acids over the aligned portions; dividing the number of identical nucleic or amino acids by the total number of nucleic or amino acids of the polynucleotide or polypeptide of the present invention; and then multiplying by 100 to determine the percentage identity. By way of example, a queried polynucleotide having 220 nucleic acids has a hit to a polynucleotide sequence in the EMBL database having 520
 20 nucleic acids over a stretch of 23 nucleotides in the alignment produced by the BLASTN algorithm using the default parameters. The 23-nucleotide hit includes 21 identical nucleotides, one gap and one different nucleotide. The percentage identity of the queried polynucleotide to the hit in the EMBL database is thus 21/220 times 100, or 9.5%. The percentage identity of polypeptide sequences may be determined in a similar fashion.

25 The BLASTN and BLASTX algorithms also produce "Expect" values for polynucleotide and polypeptide alignments. The Expect value (E) indicates the number of hits one can "expect" to see over a certain number of contiguous sequences by chance when searching a database of a certain size. The Expect value is used as a significance threshold for determining whether the hit to a database indicates true similarity. For example, an E
 30 value of 0.1 assigned to a polynucleotide hit is interpreted as meaning that in a database of the size of the EMBL database, one might expect to see 0.1 matches over the aligned portion

of the sequence with a similar score simply by chance. By this criterion, the aligned and matched portions of the sequences then have a probability of 90% of being related. For sequences having an E value of 0.01 or less over aligned and matched portions, the probability of finding a match by chance in the EMBL database is 1% or less using the
5 BLASTN algorithm. E values for polypeptide sequences may be determined in a similar fashion using various polypeptide databases, such as the SwissProt database.

According to one embodiment, "variant" polynucleotides and polypeptides, with reference to each of the polynucleotides and polypeptides of the present invention, preferably comprise sequences having the same number or fewer nucleotides or amino acids than each
10 of the polynucleotides or polypeptides of the present invention and producing an E value of 0.01 or less when compared to the polynucleotide or polypeptide of the present invention. That is, a variant polynucleotide or polypeptide is any sequence that has at least a 99% probability of being related to the polynucleotide or polypeptide of the present invention, measured as having an E value of 0.01 or less using the BLASTN or BLASTX algorithms set
15 at the default parameters. According to a preferred embodiment, a variant polynucleotide is a sequence having the same number or fewer nucleic acids than a polynucleotide of the present invention that has at least a 99% probability of being related to the polynucleotide of the present invention, measured as having an E value of 0.01 or less using the BLASTN algorithm set at the default parameters. Similarly, according to a preferred embodiment, a
20 variant polypeptide is a sequence having the same number or fewer amino acids than a polypeptide of the present invention that has at least a 99% probability of being related as the polypeptide of the present invention, measured as having an E value of 0.01 or less using the BLASTP algorithm set at the default parameters.

In an alternative embodiment, variant polynucleotides are sequences that hybridize to
25 a polynucleotide of the present invention under stringent conditions. Stringent hybridization conditions for determining complementarity include salt conditions of less than about 1 M, more usually less than about 500 mM, and preferably less than about 200 mM. Hybridization temperatures can be as low as 5°C, but are generally greater than about 22°C, more preferably greater than about 30°C, and most preferably greater than about 37°C.
30 Longer DNA fragments may require higher hybridization temperatures for specific hybridization. Since the stringency of hybridization may be affected by other factors such as

probe composition, presence of organic solvents, and extent of base mismatching, the combination of parameters is more important than the absolute measure of any one alone. An example of "stringent conditions" is prewashing in a solution of 6X SSC, 0.2% SDS; hybridizing at 65°C, 6X SSC, 0.2% SDS overnight; followed by two washes of 30 minutes
5 each in 1X SSC, 0.1% SDS at 65°C and two washes of 30 minutes each in 0.2X SSC, 0.1% SDS at 65°C.

The present invention also encompasses polynucleotides that differ from the disclosed sequences but that, as a consequence of the discrepancy of the genetic code, encode a polypeptide having similar enzymatic activity to a polypeptide encoded by a polynucleotide
10 of the present invention. Thus, polynucleotides comprising sequences that differ from the polynucleotide sequences recited in SEQ ID NO: 1-62 and 125-162, or complements, reverse sequences, or reverse complements of those sequences, as a result of conservative substitutions are contemplated by and encompassed within the present invention. Additionally, polynucleotides comprising sequences that differ from the polynucleotide
15 sequences recited in SEQ ID NO: 1-62 and 125-162, or complements, reverse complements or reverse sequences thereof, as a result of deletions and/or insertions totaling less than 10% of the total sequence length are also contemplated by and encompassed within the present invention. Similarly, polypeptides comprising sequences that differ from the polypeptide sequences recited in SEQ ID NO: 63-124 and 163-190 as a result of amino acid substitutions,
20 insertions, and/or deletions totaling less than 10% of the total sequence length are contemplated by and encompassed within the present invention, provided the variant polypeptide has activity in a lignin, fructan or tannin biosynthetic pathway.

In another aspect, the present invention provides genetic constructs comprising, in the 5'-3' direction, a gene promoter sequence; an open reading frame coding for at least a
25 functional portion of a polypeptide of the present invention; and a gene termination sequence. The open reading frame may be orientated in either a sense or anti-sense direction. For applications where amplification of lignin, fructan or tannin synthesis is desired, the open reading frame may be inserted in the construct in a sense orientation, such that transformation of a target organism with the construct will lead to an increase in the number
30 of copies of the gene and therefore an increase in the amount of enzyme. When down-regulation of lignin, fructan or tannin synthesis is desired, the open reading frame may be

inserted in the construct in an anti-sense orientation, such that the RNA produced by transcription of the polynucleotide is complementary to the endogenous mRNA sequence. This, in turn, will result in a decrease in the number of copies of the gene and therefore a decrease in the amount of enzyme. Alternatively, regulation may be achieved by inserting appropriate sequences or subsequences (*e.g.*, DNA or RNA) in ribozyme constructs.

Genetic constructs comprising a non-coding region of a gene coding for a polypeptide of the present invention, or a nucleotide sequence complementary to a non-coding region, together with a gene promoter sequence and a gene termination sequence, are also provided. As used herein the term "non-coding region" includes both transcribed sequences which are not translated, and non-transcribed sequences within about 2000 base pairs 5' or 3' of the translated sequences or open reading frames. Examples of non-coding regions which may be usefully employed in the inventive constructs include introns and 5'-non-coding leader sequences. Transformation of a target plant with such a genetic construct may lead to a reduction in the amount of lignin, fructan or tannin synthesized by the plant by the process of cosuppression, in a manner similar to that discussed, for example, by Napoli *et al.*, *Plant Cell* 2:279-290, 1990; and de Carvalho Niebel *et al.*, *Plant Cell* 7:347-358, 1995.

The genetic constructs of the present invention further comprise a gene promoter sequence and a gene termination sequence, operably linked to the polynucleotide to be transcribed, which control expression of the gene. The gene promoter sequence is generally positioned at the 5' end of the polynucleotide to be transcribed, and is employed to initiate transcription of the polynucleotide. Gene promoter sequences are generally found in the 5' non-coding region of a gene but they may exist in introns (Luehrsen, *Mol. Gen. Genet.* 225:81-93, 1991). When the construct includes an open reading frame in a sense orientation, the gene promoter sequence also initiates translation of the open reading frame. For genetic constructs comprising either an open reading frame in an anti-sense orientation or a non-coding region, the gene promoter sequence consists only of a transcription initiation site having a RNA polymerase binding site.

A variety of gene promoter sequences which may be usefully employed in the genetic constructs of the present invention are well known in the art. The promoter gene sequence, and also the gene termination sequence, may be endogenous to the target plant host or may be exogenous, provided the promoter is functional in the target host. For example, the

promoter and termination sequences may be from other plant species, plant viruses, bacterial plasmids and the like. Preferably, gene promoter and termination sequences are from the inventive sequences themselves.

Factors influencing the choice of promoter include the desired tissue specificity of the construct, and the timing of transcription and translation. For example, constitutive promoters, such as the 35S Cauliflower Mosaic Virus (CaMV 35S) promoter, will affect the activity of the enzyme in all parts of the plant. Use of a tissue specific promoter will result in production of the desired sense or anti-sense RNA only in the tissue of interest. With DNA constructs employing inducible gene promoter sequences, the rate of RNA polymerase binding and initiation can be modulated by external stimuli, such as light, heat, anaerobic stress, alteration in nutrient conditions and the like. Temporally regulated promoters can be employed to effect modulation of the rate of RNA polymerase binding and initiation at a specific time during development of a transformed cell. Preferably, the original promoters from the enzyme gene in question, or promoters from a specific tissue-targeted gene in the organism to be transformed, such as *Lolium* or *Festuca*, are used. Grass promoters different from the original gene may also be usefully employed in the inventive genetic constructs in order to prevent feedback inhibition. For example, the fructosyltransferase gene will be regulated by sucrose sensing systems; therefore removing the gene from under control of its normal promoter allows the gene to be active all the time. Other examples of gene promoters which may be usefully employed in the present invention include, mannopine synthase (mas), octopine synthase (ocs) and those reviewed by Chua *et al.*, *Science* 244:174-181, 1989.

The gene termination sequence, which is located 3' to the polynucleotide to be transcribed, may come from the same gene as the gene promoter sequence or may be from a different gene. Many gene termination sequences known in the art may be usefully employed in the present invention, such as the 3' end of the *Agrobacterium tumefaciens* nopaline synthase gene. However, preferred gene terminator sequences are those from the original enzyme gene or from the target species to be transformed.

The genetic constructs of the present invention may also contain a selection marker that is effective in plant cells, to allow for the detection of transformed cells containing the inventive construct. Such markers, which are well known in the art, typically confer

resistance to one or more toxins. One example of such a marker is the NPTII gene whose expression results in resistance to kanamycin or hygromycin, antibiotics which are usually toxic to plant cells at a moderate concentration (Rogers *et al.*, in Weissbach A and H, eds., *Methods for Plant Molecular Biology*, Academic Press Inc.: San Diego, CA, 1988).

5 Alternatively, the presence of the desired construct in transformed cells can be determined by means of other techniques well known in the art, such as Southern and Western blots.

Techniques for operatively linking the components of the inventive genetic constructs are well known in the art and include the use of synthetic linkers containing one or more restriction endonuclease sites as described, for example, by Sambrook *et al.*, (*Molecular cloning: a laboratory manual*, CSHL Press: Cold Spring Harbor, NY, 1989). The genetic
10 construct of the present invention may be linked to a vector having at least one replication system, for example, *E. coli*, whereby after each manipulation, the resulting construct can be cloned and sequenced and the correctness of the manipulation determined.

The genetic constructs of the present invention may be used to transform a variety of
15 plants, both monocotyledonous (*e.g.*, grasses, maize/corn, grains, oats, rice, sorghum, millet, rye, sugar cane, wheat and barley), dicotyledonous (*e.g.*, *Arabidopsis*, tobacco, legumes, alfalfa, oaks, eucalyptus, maple), and gymnosperms. In a preferred embodiment, the inventive genetic constructs are employed to transform grasses. Preferably the target plant is selected from the group consisting of *Lolium* and *Festuca* species, most preferably from the
20 group consisting of *Lolium perenne* and *Festuca arundinacea*. Other plants that may be usefully transformed with the inventive genetic constructs include other species of ryegrass and fescue, including, but not limited to *Lolium multiflorum* (Italian ryegrass), *Lolium hybridum* (hybrid ryegrass), *Lolium rigidum* (Wimmera grass), *Lolium temulentum* (darnel), *Festuca rubra* (red fescue) and *Festuca pratensis* (meadow fescue). As discussed above,
25 transformation of a plant with a genetic construct of the present invention will produce a modified lignin, fructan or tannin content in the plant.

The production of RNA in target cells may be controlled by choice of the promoter sequence, or by selecting the number of functional copies or the site of integration of the polynucleotides incorporated into the genome of the target organism. A target plant may be
30 transformed with more than one construct of the present invention, thereby modulating the lignin, fructan and/or tannin biosynthetic pathways by affecting the activity of more than one

enzyme, affecting enzyme activity in more than one tissue or affecting enzyme activity at more than one expression time. Similarly, a construct may be assembled containing more than one open reading frame coding for an enzyme encoded by a polynucleotide of the present invention or more than one non-coding region of a gene coding for such an enzyme.

- 5 The polynucleotides of the present invention may also be employed in combination with other known sequences encoding enzymes involved in the lignin, fructan and/or tannin biosynthetic pathways. In this manner, more than one biosynthetic pathway may be modulated, or a lignin, fructan or tannin biosynthetic pathway may be added to a plant to produce a plant having an altered phenotype.

- 10 Techniques for stably incorporating genetic constructs into the genome of target plants are well known in the art and include *Agrobacterium tumefaciens* mediated introduction, electroporation, protoplast fusion, injection into reproductive organs, injection into immature embryos, high velocity projectile introduction and the like. The choice of technique will depend upon the target plant to be transformed. For example, dicotyledonous
- 15 plants and certain monocots and gymnosperms may be transformed by *Agrobacterium* Ti plasmid technology, as described, for example by Bevan, *Nucleic Acid Res.* 12:8711-8721, 1984. Targets for the introduction of the genetic constructs of the present invention include tissues, such as leaf tissue, disseminated cells, protoplasts, seeds, embryos, meristematic regions; cotyledons, hypocotyls, and the like. Transformation techniques which may be
- 20 usefully employed in the inventive methods include those taught by Ellis *et al.*, *Plant Cell Reports*, 8:16-20, 1989; Wilson *et al.*, *Plant Cell Reports* 7:704-707, 1989; Tautorius *et al.*, *Theor. Appl. Genet.* 78:531-536, 1988; Hiei *et al.*, *Plant J.* 6:271-282, 1994; and Ishida *et al.*, *Nature Biotechnol.* 14:745-750, 1996; US Patent 5,591,616; and European Patent Publication EP 672 752 A1. Once the cells are transformed, cells having the inventive DNA construct
- 25 incorporated in their genome may be selected by means of a marker, such as the kanamycin resistance marker discussed above. Transgenic cells may then be cultured in an appropriate medium to regenerate whole plants, using techniques well known in the art. In the case of protoplasts, the cell wall is allowed to reform under appropriate osmotic conditions. In the case of seeds or embryos, an appropriate germination or callus initiation medium is
- 30 employed. For explants, an appropriate regeneration medium is used. Regeneration of plants is well established for many species. The resulting transformed plants may be reproduced

sexually or asexually, using methods well known in the art, to give successive generations of transgenic plants.

Polynucleotides of the present invention may also be used to specifically suppress gene expression by methods that operate post-transcriptionally to block the synthesis of products of targeted genes, such as RNA interference (RNAi), and quelling. For a review of techniques of gene suppression see *Science*, 288:1370-1372, 2000. Exemplary gene silencing methods are also provided in WO 99/49029 and WO 99/53050. Posttranscriptional gene silencing is brought about by a sequence-specific RNA degradation process which results in the rapid degradation of transcripts of sequence-related genes. Studies have provided evidence that double-stranded RNA may act as a mediator of sequence-specific gene silencing (see, e.g., review by Montgomery and Fire, *Trends in Genetics*, 14: 255-258, 1998). Gene constructs that produce transcripts with self-complementary regions are particularly efficient at gene silencing. A unique feature of this posttranscriptional gene silencing pathway is that silencing is not limited to the cells where it is initiated. The gene silencing effects may be disseminated to other parts of an organism and even transmitted through the germ line to several generations.

The polynucleotides of the present invention may be employed to generate gene silencing constructs and or gene-specific self-complementary RNA sequences that can be delivered by conventional art-known methods to plant tissues, such as forage grass tissues. Within genetic constructs, sense and antisense sequences can be placed in regions flanking an intron sequence in proper splicing orientation with donor and acceptor splicing sites, such that intron sequences are removed during processing of the transcript and sense and antisense sequences, as well as splice junction sequences, bind together to form double-stranded RNA. Alternatively, spacer sequences of various lengths may be employed to separate self-complementary regions of sequence in the construct. During processing of the gene construct transcript, intron sequences are spliced-out, allowing sense and anti-sense sequences, as well as splice junction sequences, to bind forming double-stranded RNA. Select ribonucleases bind to and cleave the double-stranded RNA, thereby initiating the cascade of events leading to degradation of specific mRNA gene sequences, and silencing specific genes. Alternatively, rather than using a gene construct to express the self-complementary RNA sequences, the gene-specific double-stranded RNA segments are

delivered to one or more targeted areas to be internalized into the cell cytoplasm to exert a gene silencing effect. Gene silencing RNA sequences comprising the polynucleotides of the present invention are useful for creating genetically modified plants with desired phenotypes as well as for characterizing genes (e.g., in high-throughput screening of sequences), and
5 studying their functions in intact organisms.

Example 1

ISOLATION OF CDNA SEQUENCES FROM *L. PERENNE* AND *F. ARUNDINACEA* CDNA LIBRARIES

10 *L. perenne* and *F. arundinacea* cDNA expression libraries were constructed and screened as follows. Tissue was collected from *L. perenne* and *F. arundinacea* during winter and spring, and snap-frozen in liquid nitrogen. The tissues collected include those obtained from leaf blades, leaf base, pseudostem, floral stems, inflorescences, roots and stem. Total
15 RNA was isolated from each tissue type using TRIzol Reagent (BRL Life Technologies, Gaithersburg, MD). mRNA from each tissue type was obtained using a Poly(A) Quik mRNA isolation kit (Stratagene, La Jolla, CA), according to the manufacturer's specifications. cDNA expression libraries were constructed from the purified mRNA by reverse transcriptase synthesis followed by insertion of the resulting cDNA in Lambda ZAP
20 using a ZAP Express cDNA Synthesis Kit (Stratagene, La Jolla, CA), according to the manufacturer's protocol. The resulting cDNA clones were packaged using a Gigapack II Packaging Extract (Stratagene, La Jolla, CA) employing 1 µl of sample DNA from the 5 µl ligation mix. Mass excision of the libraries was done using XL1-Blue MRF' cells and XL0LR cells (Stratagene, La Jolla, CA) with ExAssist helper phage (Stratagene, La Jolla,
25 CA). The excised phagemids were diluted with NZY broth (Gibco BRL, Gaithersburg, MD) and plated out onto LB-kanamycin agar plates containing 5-bromo-4-chloro-3-indolyl-beta-D-galactosidase (X-gal) and isopropylthio-beta-galactoside (IPTG). Of the colonies plated and picked for DNA preparations, the large majority contained an insert suitable for sequencing. Positive colonies were cultured in NZY broth with kanamycin and DNA was
30 purified following standard protocols. Agarose gel at 1% was used to screen sequencing templates for chromosomal contamination. Dye terminator sequences were prepared using a

Biomek 2000 robot (Beckman Coulter Inc., Fullerton, CA) for liquid handling and DNA amplification using a 9700 PCR machine (Perkin Elmer/Applied Biosystems, Foster City, CA) according to the manufacturer's protocol.

The DNA sequences for positive clones were obtained using a Perkin Elmer/Applied Biosystems Division Prism 377 sequencer. cDNA clones were sequenced from the 5' end. The polynucleotide sequences identified as SEQ ID NO: 4, 6, 11, 127, 128 and 132 were identified from *L. perenne* leaf cDNA expression libraries; the polynucleotide sequences identified as SEQ ID NO: 1, 14, 15, 26, 32, 36, 38, 41, 49, 125, 134, 141, 144, 147, and 150 were identified from *L. perenne* vegetative stem cDNA expression libraries; the polynucleotide sequences identified as SEQ ID NO: 17, 22, 25, 138, and 140 were identified from *L. perenne* leaf and pseudostem cDNA expression libraries; the polynucleotide sequences identified as SEQ ID NO: 43, 57, 61, 157, and 161 were identified from *L. perenne* pseudostem cDNA expression libraries; the polynucleotide sequences identified as SEQ ID NO: 10, 12, 28, 30, 34, 44, 60, 131, 133, 142, 143, 145, 151, and 160 were identified from *L. perenne* floral stem cDNA expression libraries; the polynucleotide sequences identified as SEQ ID NO: 8, 18, 46, 52, 53, 55, 59, 136, 152, 155, 156, 159, and 162 were identified from *L. perenne* stem cDNA expression libraries; the polynucleotide sequences identified as SEQ ID NO: 51 and 154 were identified from a *L. perenne* root cDNA expression library; the polynucleotide sequences identified as SEQ ID NO: 24, 27 and 139 were identified from *L. perenne* leaf blade cDNA expression libraries; the polynucleotide sequences identified as SEQ ID NO: 9, 37, 39, 40, 45, 130, 148, and 149 were identified from *F. arundinacea* basal leaf cDNA expression libraries; the polynucleotide sequences identified as SEQ ID NO: 19, 21, 29, 33, 35, 47, 48, and 153 were identified from *F. arundinacea* combined day 3 and day 6 basal leaves cDNA expression libraries; the polynucleotide sequence identified as SEQ ID NO: 54 was identified from a *F. arundinacea* combined day 3 and day 6 leaves cDNA expression library; the polynucleotide sequence identified as SEQ ID NO: 56 was identified from a *F. arundinacea* inflorescence cDNA expression library; the polynucleotide sequences identified as SEQ ID NO: 20 and 137 were identified from a subtracted *F. arundinacea* leaf blade cDNA expression library; the polynucleotide sequences identified as SEQ ID NO: 7, 23, 42, 50, 62, and 129 were identified from *F. arundinacea* pseudostem cDNA expression libraries; the polynucleotide

sequences identified as SEQ ID NO: 2, 13, 16 and 135 were identified from *F. arundinacea* leaf cDNA expression libraries; and the polynucleotide sequences identified as SEQ ID NO: 3, 5, 31, and 126 were identified from a *F. arundinacea* inflorescence day 0 cDNA expression library.

5

BLASTN Polynucleotide Analysis

The isolated cDNA sequences were compared to sequences in the EMBL DNA database using the computer algorithm BLASTN. Comparisons of DNA sequences provided in SEQ ID NOS: 1-62 to sequences in the EMBL DNA database were made as of October 19, 2001 using BLASTN algorithm Version 2.0.11 [Jan-20-2000], and the following Unix running command: blastall -p blastn -d embldb -e 10 -G0 -E0 -r 1 -v 30 -b 30 -i queryseq -o. Comparisons of DNA sequences provided in SEQ ID NOS: 125-162 to sequences in the EMBL DNA database were made using BLASTN algorithm Version 2.2.1 [Apr-13-2001], and the following Unix running command: blastall -p blastn -d embldb -F F -e 10 -G0 -E0 -r 1 -v 2 -b 2 -i queryseq -o.

The sequences of SEQ ID NO: 4-6, 9-11, 17-19, 21-26, 33, 44, 45, 48, 49, 51-55, 59, 60, 130-132, 136, 139, 146, 151, 154-156, 159, and 162 were determined to have less than 50% identity to sequences in the EMBL database using the computer algorithm BLASTN, as described above. The sequences of SEQ ID NO: 2, 3, 7, 8, 14, 16, 36-38, 46, 47, 50, 56-58, 61, 129, 135, 137, 138, 152, 153, 157, 158, 160 and 161 were determined to have less than 75% identity to sequences in the EMBL database using the computer algorithm BLASTN, as described above. The sequences of SEQ ID NOS: 1, 12, 13, 15, 20, 28, 31, 32, 35, 40 62, 125-128, 133, 134, 142, 144 and 147 were determined to have less than 90% identity to sequences in the EMBL database using the computer algorithm BLASTN, as described above. Finally, the sequences of SEQ ID NOS: 29, 30, 39, 41-43, 141, 143, 148, and 149 were determined to have less than 98% identity to sequences in the EMBL database using the computer algorithm BLASTN, as described above.

BLASTP Polypeptide Analysis

The protein sequences corresponding to the isolated cDNA sequences were compared to sequences in the SwissProt/Trembl protein database using the computer algorithm

BLASTP. Comparisons of protein sequences provided in SEQ ID NOS: 63-124 to sequences in the SwissProt/Trembl protein database were made as of October 19, 2001 using BLASTP algorithm Version 2.0.11 [Jan-20-2000], and the following Unix running command: blastall -p blastp -dstdb-e 10 -G0 -E0 -v 30 -b 30 -i queryseq -o. Comparisons of protein sequences provided in SEQ ID NOS: 163-190 to sequences in the SwissProt/Trembl protein database were made using BLASTP algorithm Version 2.2.1 [Apr-13-2001], and the following Unix running command: blastall -p blastp -d stdb -F F -e 10 -G0 -E0 -v 2 -b 2 -i queryseq -o.

The sequences of SEQ ID NOS: 65-68, 72, 73, 78, 80, 81, 84, 85, 87, 88, 106, 107, 110, 111, 113-115, 117, 118 and 121 were determined to have less than 50% identity to sequences in the SwissProt/Trembl database using the computer algorithm BLASTP, as described above. The sequences of SEQ ID NOS: 71, 79, 82, 83, 86, 95, 98-100, 112, 116, 120, 122-124, 167, 168, 171-174, 185, 188, and 190 were determined to have less than 75% identity to sequences in the SwissProt/Trembl database using the computer algorithm BLASTP, as described above. The sequences of SEQ ID NOS: 63, 64, 69, 70, 74-77, 90, 91, 93, 94, 97, 101, 102, 104, 108, 109, 119, 175, 183, 187, and 189 were determined to have less than 90% identity to sequences in the SwissProt/Trembl database using the computer algorithm BLASTP, as described above. Finally, the sequences of SEQ ID NOS: 89, 92, 96, 103, 105, 163-165, 169, 170, 177, 179, 181, 184, and 186 were determined to have less than 98% identity to sequences in the SwissProt/Trembl database using the computer algorithm BLASTP, as described above.

BLASTX Polynucleotide Analysis

The isolated cDNA sequences were compared to sequences in the SwissProt/Trembl protein database using the computer algorithm BLASTX. Comparisons of DNA sequences provided in SEQ ID NOS: 1-62 to sequences in the SwissProt/Trembl protein database were made as of October 19, 2001 using BLASTX algorithm Version 2.0.11 [Jan-20-2000], and the following Unix running command: blastall -p blastx -dstdb -e 10 -G0 -E0 -v 30 -b 30 -i queryseq -o. Comparisons of DNA sequences provided in SEQ ID NOS: 1-62 to sequences in the SwissProt/Trembl protein database were made using BLASTX algorithm

Version 2.2.1 [Apr-13-2001], and the following Unix running command: blastall -p blastx -d stdb -F F -e 10 -G0 -E0 -v 2 -b 2 -i queryseq -o.

The sequences of SEQ ID NOS: 11, 44, 45, 48, 49, 51, 52, 55, 130, 132, 155, 156, and 162 were determined to have less than 50% identity to sequences in the SwissProt/Trembl database using the computer algorithm BLASTX, as described above. The sequences of SEQ ID NOS: 3-10, 16-26, 33, 36-38, 40-43, 50, 53, 54, 56, 58-62, 129, 131, 135-139, 146, 150, 151, 154, and 158-161 were determined to have less than 75% identity to sequences in the SwissProt/Trembl database using the computer algorithm BLASTX, as described above. The sequences of SEQ ID NOS: 1, 2, 12-15, 27, 28-32, 34, 35, 39, 46, 47, 57, 125-128, 133, 134, 141-145, 147-149, 152, 153, and 157 were determined to have less than 90% identity to sequences in the SwissProt/Trembl database using the computer algorithm BLASTX, as described above. Finally, the sequence of SEQ ID NO: 140 was determined to have less than 98% identity to sequences in the SwissProt/Trembl database using the computer algorithm BLASTX, as described above.

The location of open reading frames (ORFs), by nucleotide position, contained within the sequences of SEQ ID NO: 1-62 and 125-162, and the corresponding amino acid sequences are provided in Table 2 below. SEQ ID NO: 1-8, 10-15, 17, 19, 21, 23-25, 28-52, 54-59, 61-62 and 125-162 are believed to contain full-length ORFs.

TABLE 2

POLYNUCLEOTIDE SEQ ID NO:	ORF	POLYPEPTIDE SEQ ID NO:
1	56-2,020	63
2	64-2,010	64
3	64-1,926	65
4	74-1,945	66
5	40-1,911	67
6	79-1,938	68
7	246-1,514	69
8	264-1,532	70
9	84-3,272	71
10	73-3,297	72
11	129-2,942	73
12	46-2,472	74
13	113-2,539	75
14	61-2,505	76

POLYNUCLEOTIDE SEQ ID NO:	ORF	POLYPEPTIDE SEQ ID NO:
15	103-2,253	77
16	3-1,439	78
17	26-1,777	79
18	2-1,174	80
19	59-1,852	81
20	2-1,201	82
21	1-1,779	83
22	198-1,097	84
23	27-1,772	85
24	36-1,802	86
25	78-2,084	87
26	2-1,423	88
27	3-1,622	89
28	85-1,764	90
29	72-1,751	91
30	127-1,800	92
31	137-1,810	93
32	62-1,567	94
33	80-1,597	95
34	32-1,117	96
35	86-1,171	97
36	55-852	98
37	75-872	99
38	149-1,240	100
39	90-1,118	101
40	28-1,110	102
41	66-1,148	103
42	64-1,146	104
43	85-1,170	105
44	88-1,683	106
45	93-1,721	107
46	111-2,246	108
47	144-2,285	109
48	22-993	110
49	4-1,038	111
50	87-1,067	112
51	59-1,135	113
52	18-1,052	114
53	1-882	115
54	80-1,015	116
55	322-1,014	117
56	172-762	118
57	118-1,299	119

POLYNUCLEOTIDE SEQ ID NO:	ORF	POLYPEPTIDE SEQ ID NO:
58	5-595	120
59	14-1,003	121
60	1-987	122
61	65-1,174	123
62	103-1,245	124
125	55-2,019	163
126	63-1,925	164
127	73-1,944	165
128	71-1,930	166
131	72-3,299	167
132	134-2,950	168
133	45-2,471	169
134	65-2,512	170
135	74-1,819	171
136	170-1,855	172
137	28-1,770	173
138	26-1,733	174
139	35-1,801	175
140	71-2,083	176
141	63-1,607	177
143	126-1,799	178
144	61-1,566	179
145	67-1,152	180
147	148-1,239	181
149	27-1,109	182
151	87-1,718	183
153	143-2,284	184
156	46-1,017	185
157	117-1,313	186
158	81-1,193	187
159	12-1,001	188
160	26-1,018	189
162	50-1,027	190

SEQ ID NO: 125 and 163 are related to SEQ ID NO: 1 and 63, respectively; SEQ ID NO: 126 and 164 are related to SEQ ID NO: 3 and 65, respectively; SEQ ID NO: 127 and 165 are related to SEQ ID NO: 4 and 66, respectively; SEQ ID NO: 128 and 166 are related to SEQ ID NO: 6 and 68, respectively; SEQ ID NO: 129 is an extended sequence of SEQ ID NO: 7; SEQ ID NO: 130 is an extended sequence of SEQ ID NO: 9; SEQ ID NO: 131 and 167 are related to SEQ ID NO: 10 and 72, respectively; SEQ ID NO: 132 and 168 are related

to SEQ ID NO: 11 and 73, respectively; SEQ ID NO: 133 and 169 are related to SEQ ID NO: 12 and 74, respectively; SEQ ID NO: 134 and 170 are related to SEQ ID NO: 14 and 76, respectively; SEQ ID NO: 135 and 171 are full-length sequences of SEQ ID NO: 16 and 78, respectively; SEQ ID NO: 136 and 172 are full-length sequences of SEQ ID NO: 18 and 80, respectively; SEQ ID NO: 137 and 173 are related to SEQ ID NO: 20 and 82, respectively; SEQ ID NO: 138 and 174 are full-length sequences of SEQ ID NO: 22 and 84, respectively; SEQ ID NO: 139 and 175 are related to SEQ ID NO: 24 and 86, respectively; SEQ ID NO: 140 and 176 are related to SEQ ID NO: 25 and 87, respectively; SEQ ID NO: 141 and 177 are full-length sequences of SEQ ID NO: 26 and 88, respectively; SEQ ID NO: 142 is related to SEQ ID NO: 28 and encodes the same amino acid sequence; SEQ ID NO: 143 and 178 are related to SEQ ID NO: 30 and 92, respectively; SEQ ID NO: 144 and 179 are related to SEQ ID NO: 32 and 94, respectively; SEQ ID NO: 145 and 180 are full-length sequences of SEQ ID NO: 34 and 96, respectively; SEQ ID NO: 146 is related to SEQ ID NO: 36 and encodes the same amino acid sequence; SEQ ID NO: 147 and 181 are related to SEQ ID NO: 38 and 100, respectively; SEQ ID NO: 148 is related to SEQ ID NO: 39, and encodes the same amino acid sequence; SEQ ID NO: 149 and 182 are related to SEQ ID NO: 40 and 102, respectively; SEQ ID NO: 150 is related to SEQ ID NO: 41 and encodes the same amino acid sequence; SEQ ID NO: 151 and 183 is related to SEQ ID NO: 44 and 106, respectively; SEQ ID NO: 152 is related to SEQ ID NO: 46, and encodes the same amino acid sequence; SEQ ID NO: 153 and 184 are related to SEQ ID NO: 47 and 109, respectively; SEQ ID NO: 154 is related to SEQ ID NO: 51, and encodes the same amino acid sequence; SEQ ID NO: 155 is related to SEQ ID NO: 52, and encodes the same amino acid sequence; SEQ ID NO: 156 and 185 are full-length sequences of SEQ ID NO: 53 and 115, respectively; SEQ ID NO: 162 and 190 are variants of SEQ ID NO: 156 and 185, respectively, with a difference in the 5' region of SEQ ID NO: 156 and 162; SEQ NO: 157 and 186 are related to SEQ ID NO: 57 and 119, respectively; SEQ ID NO: 158 and 187 are related to SEQ ID NO: 58 and 120, respectively; SEQ ID NO: 159 and 188 are full-length sequences of SEQ ID NO: 59 and 121, respectively; SEQ ID NO: 160 and 189 are full-length sequences of SEQ ID NO: 60 and 122, respectively; and SEQ ID NO: 161 is related to SEQ ID NO: 61 and encodes the same amino acid sequence.

Example 2

USE OF SUCROSE PHOSPHATE PHOSPHATASE TO DEPHOSPHORYLATE SUCROSE-6-PHOSPHATE

The *F. arundinacea* and *L. perenne* FaSPP and LpSPP genes (SEQ ID NO: 7 and 8, respectively) share amino acid sequence identity with sucrose-6-phosphate phosphatase genes from other plant species (Lunn *et al.*, *Proc. Natl. Acad. Sci. USA* 97:12914-12919, 2000). These genes were amplified by PCR using the primers given in SEQ ID NO: 191 and 192 to add an initiating methionine, and then cloned into the pET41a expression plasmid. These primers amplified nucleotides 263-1531 and 280-1548 for FaSPP and LpSPP, respectively. The resulting plasmids were transformed into *E. coli* BL21 cells using standard protocols, and protein expression was induced using IPTG.

The soluble recombinant protein was assayed for its ability to specifically dephosphorylate sucrose-6-phosphate (Suc-6-P) but not fructose-6-phosphate (Fru-6-P) using the procedure described by Lunn *et al.* (*ibid.*). The release of phosphate from Suc-6P and Fru-6-P was measured using the Fiske-Subbarow method of determining inorganic phosphate (SIGMA assay kit; Sigma, St Louis, MI), with the change in absorbance at 660 nm being proportional to the amount of phosphate released per unit time. As shown in Fig. 1, both the *Festuca* and *Lolium* SPP enzymes dephosphorylated Suc-6-P but not Fru-6-P, whereas control pET41 extract had no activity on either substrate.

20

Example 3

PEROXIDASE ACTIVITY OF GRASS ENZYMES DEMONSTRATED BY THEIR ABILITY TO OXIDIZE

2,2'AZINO-BIS.3-ETHYLBENZYLTHIAZOLINE-6-SULFONIC ACID (ABTS)

25

A number of *L. perenne* or *F. arundinacea* genes (SEQ ID NO: 48 – 54) share amino acid identity with peroxidase genes from other plant species (Hiraga *et al.*, *Plant Cell Physiol.* 42:462-468, 2001). The putative amino acid secretion signal sequence was identified by signalP analysis of the *Lolium* and *Festuca* sequences and homology to known peroxidase proteins. Primers were designed to amplify DNA representing the mature protein (minus signal sequence; Table 3.). These genes were amplified by PCR to add an initiating methionine and then cloned into the pET25b expression plasmid. The resulting plasmid was

transformed into *E. coli* AD494 (DE3) pLysS cells using standard protocols, and protein expression was induced using IPTG.

TABLE 3

SEQ ID NO DNA	SEQ ID NO PROT	Gene	Primers SEQ ID NO:	DNA bp amplified	Protein codons
50	112	FaPER3	193 194	156-1077	24-326
52	114	LpPER5	195 196	120-1052	35-344

5

The insoluble recombinant protein was solubilized and re-folded following protocols described for several recombinant *Arabidopsis* peroxidases (Teilum *et al.*, *Protein Exp. and Purif.* 15:77-82, 1999). The insoluble inclusion bodies within *E. coli* were isolated from
 10 lysed cells by standard protocols and the recombinant protein solubilized in 8M urea. The solubilized peroxidase protein was refolded to gain active enzyme by diluting urea to 2M with 5μM Heme, 0.25mM Glutathione reduced, and 0.45mM Glutathione oxidized, pH 8 (20mM Tris-HCl). The refolded protein was used directly to assay peroxidase activity.

Peroxidase activity was measured by incubating recombinant peroxidase with pre-
 15 mixed ABTS/H₂O₂ liquid substrate (Sigma, St Louis, MI) and measuring ABTS oxidation by the increase in absorbance at 405nm. Horseradish peroxidase of known activity (Sigma, St Louis, MI) was used as a positive control and boiled samples as a negative control. The results provided in Fig. 2 show that FaPER3 and LpPER5 (SEQ ID NO: 50 and 52, respectively) had similar activity to that of horseradish peroxidase in these assays.

20

Example 4

USE OF GRASS FRUCTOSYLTRANSFERASE GENES TO SYNTHESIZE FRUCTANS

Transformation of *N. benthamiana* plants with fructosyltransferase genes

25 Sense constructs containing a polynucleotide including the coding region of fructosyltransferase genes isolated from *L. perenne* Lp1-SST and Lp6SFT1 (SEQ ID NO: 125 and 126, respectively) were inserted into a pART27 derived binary vector and used to

transform *A. tumefaciens* LBA4404 using published methods (*see, An et al.*, "Binary Vectors," in Gelvin and Schilperoort, eds., *Plant Molecular Biology Manual*, Kluwer Academic Publishers: Dordrecht, 1988). The presence and integrity of the binary vector in *A. tumefaciens* was verified by polymerase chain reaction (PCR). The primers px17 (SEQ ID NO: 207) and px18 (SEQ ID NO: 208) were used to confirm the presence of the Lp1-SST construct; whereas the primers px19 (SEQ ID NO: 209) and px 20 (SEQ ID NO: 210) were used to confirm the presence of the Lp6-SFT-1 construct.

The *A. tumefaciens* containing the sense gene constructs were used to transform *N. benthamiana* leaf discs (Burow *et al.*, *Plant Mol. Biol. Report* 8:124-139, 1990). Several independent transformed plant lines were established for the sense construct for each fructosyltransferase gene. DNA was isolated from transformed plants containing the appropriate fructosyltransferase gene construct using the QIAGEN DNAeasy Plant Mini Kit (Qiagen, Valencia, CA). Presence of the fructosyltransferase gene was verified using PCR experiments as shown in Figs. 3 and 4. For the Lp6-SFT1 gene, the forward and reverse primers given in SEQ ID NO: 197 and 198 were used, respectively. These primers amplify nucleotides 1572 - 1980 of the Lp6-SFT1 gene which corresponds to a 406 base pair fragment. For Lp1-SST, the forward and reverse primers given in SEQ ID NO: 199 and 200 were used, respectively. These primers amplify nucleotides 1332 - 1740 of Lp1-SST, corresponding to a 414 base pair fragment.

Effects of fructosyltransferase genes on fructosyltransferase concentration in transformed plants

Fructans are not normally found in *N. benthamiana* plants; hence, if introduction of the sense fructosyltransferase constructs was successful, it should be possible to extract fructans from the transformed plants. The concentration of fructosyltransferase in the transformed plants was determined using the Fructan Assay Kit (Megazyme International Ireland Ltd, Wicklow, Ireland). Briefly, 300 mg of leaf material from the independent transformed plant lines containing the fructosyltransferase sense constructs were extracted individually at 80 °C with 1 ml 80% ethanol, followed by two 1 ml extractions with water. The ethanol and water extracts were combined and frozen overnight at -20 °C. Extracts were centrifuged at 20,000 g to pellet chlorophyll. Clarified extracts were treated with 1%

PVP-40 to precipitate phenolic compounds. These extracts were then reduced in volume by rotary evaporation.

Fructan levels were determined in these extracts using the Megazyme Fructan Assay kit. Briefly, sucrose, starch and reducing sugars are removed from the plant carbohydrate extracts by using sucrase, β -amylase, pullulanase and maltase, and then converting the resulting reducing sugars to sugar alcohols. The remaining fructans are hydrolyzed with fructanase and the reducing sugars produced (glucose and fructose) are measured by the 4-hydroxybenzoic acid hydrazide (PAHBAH) reducing sugar method. The final extracts are assayed for absorbance at 410 nm. As shown in Fig. 5, fructans could be detected in both the Lp1-SST and Lp6-SFT-1 transgenic lines. Fructan levels were highest in lines 07, 09 and 12 for Lp1-SST, and lines 05 and 12 for Lp6SFT-1.

Example 5

USE OF SUCROSE PHOSPHATE SYNTHASE ENZYMES TO SYNTHESIZE SUCROSE

A *F. arundinacea* gene (FaSPS-N; SEQ ID NO: 9) has been identified that shares amino acid sequence identity with sucrose phosphate synthase (SPS) from other plant species. SEQ ID NO: 7 and 8 are also SPS sequences, with SEQ ID NO: 7 being a *Lolium perenne* homologue of SEQ ID NO: 9. The FaSPS-N was cloned into the pcDNA3 mammalian expression plasmid and the resulting plasmid transfected into 293T mammalian cells (human embryonic kidney derived cells) using Lipofectamine 2000 reagent (Invitrogen, Carlsbad, CA).

Cell lysates from transfected cells were deionized on G25 spin columns and used in a sucrose synthesis assay. In this assay, mammalian cell extracts were tested for their ability to synthesize sucrose from fructose-6-phosphate and uridine 5'-diphosphoglucose. Following the synthesis reaction, hexoses were converted to sugar alcohols by boiling in the presence of 30% KOH. The sucrose synthesized was detected by the addition of 1.4 % anthrone reagent in H_2SO_4 and incubating at 40 °C for 20 min. The change in absorbance at 620 nm is relative to sucrose in the reaction (Botha and Black, *Aust. J. Plant Physiol.* 27:81-85, 2000). In these experiments, introducing FaSPS-N alone into mammalian cells produced a sucrose synthesis activity that was not detected in non-transfected cells (Fig. 6).

A known cofactor for SPS is SPP. To test whether SPP is required for SPS activity, the *L. perenne* LpSPP gene (SEQ ID NO: 8) was cloned into the pcDNA3 mammalian expression plasmid. Both the FaSPS-N and LpSPP plasmids were co-transfected into 293T mammalian cells using Lipofectamine 2000 reagent (Invitrogen, Carlsbad, CA). Cell lysates
5 from transfected cells were deionized on G25 spin columns and used in a sucrose synthesis assay as described above. As shown in Fig. 6, adding SPP did not significantly enhance or alter the sucrose synthesis activity of the cell extracts.

Example 6

10 USE OF SOLUBLE SUCROSE SYNTHASE ENZYMES TO CLEAVE SUCROSE

A *F. arundinacea* gene (FaSUS-1; SEQ ID NO: 13) was identified that shared amino acid sequence identity with soluble sucrose synthase enzymes (SUS) from other plant species. The FaSUS-1 gene was cloned into the pcDNA3 mammalian expression plasmid,
15 which was transiently transfected into 293T mammalian cells (human embryonic kidney derived cells) using Lipofectamine 2000 reagent (Invitrogen Carlsbad, CA). Transfected cells were grown for several days before harvesting (by scraping cells in a sucrose synthase buffer). Harvested cells were frozen on dry ice and freeze-thawed twice before pelleting cell debris by centrifugation. The resulting supernatant (cell lysate) was deionized on G25 spin
20 columns and then used in a sucrose cleavage assay as described by Sebkova *et al.* (*Plant Physiol.* 108:75-83, 1995). In these assays, the cell lysates were tested for their ability to cleave sucrose in the presence of UDP to produce fructose and uridine 5'-diphosphoglucose. Following a 30 min incubation at 30 °C, the enzyme activity was stopped by boiling the tubes for 1 min. Both NAD and UDP-glucose dehydrogenase were added and the change in OD at
25 340 nM (production of NADPH) was measured. As shown in Fig. 7, significantly higher levels of sucrose cleavage were observed in cells transfected with FaSUS1 construct than in non-transfected control cells.

Example 7USE OF ACID INVERTASES TO CLEAVE SUCROSE

A number of acid (vacuolar and cell wall) invertase genes from *L. perenne* and *F. arundinacea* (SEQ ID NOS: 17, 19, 21, 23 and 135-141) were identified that share amino acid sequence identity with acid invertases from other plant species (Unger *et al.*, *Plant Physiol.* 104:1351-1357, 1994; Goetz and Roitsch, *J. Plant Physiol.* 157:581-585, 2000). These sequences were analysed by SignalP and homology to identify signal regions and propeptide sequences, and primers were designed to amplify the DNA sequence encoding the mature protein (Table 4).

TABLE 4

SEQ ID NO DNA	SEQ ID NO PROT	Gene	Primers SEQ ID NO	DNA bp amplified	Protein codons
17	79	LpCWINV1	201 202	137-1803	38-583
19	81	FaCWINV4	203 204	134-1912	26-597
25	87	LpSINV1	205 206	387-2124	104-668

The PCR fragments were cloned into pPICZ α A vectors for expression in methylotrophic yeast *Pichia pastoris* (EasySelect™ *Pichia* Expression Kit, Invitrogen, Carlsbad, CA). The sequences were cloned in frame with the α -mating factor for secretion of the recombinant invertase protein into liquid media, following similar methods described for the expression of barley 6-SFT and fescue 1-SST in *P. pastoris* (Hochstrasser *et al.*, *FEBS Letters* 440:356-360, 1998; Lüscher *et al.*, *Plant Physiol.*, 124:1217-1227, 2000). The media was concentrated 10 fold by Vivaspin 30 kDa spin column (VivaScience, Hannover, Germany) to concentrate recombinant protein and used directly to assay invertase activity. Recombinant protein was assayed with 100mM sucrose in 500 μ l phosphate buffer pH5.0, at 30 °C for 1 hour. Release of glucose by invertase activity was measured using a glucose HK assay kit (Sigma, St Louis, MI). Fig. 8 shows the glucose released by invertase activity in terms of glucose concentration in the assay mix. As shown in Fig. 8, invertase activity was observed for the vacuolar invertase (LpSINV1; SEQ NO: 25) and the two cell wall invertases

(LpCWINV1 and FaCWINV4; SEQ NO: 17 and 19, respectively) but not for an empty vector (pPICZalphaA) control.

Example 8

5

USE OF TANNIN GENES TO MODIFY TANNIN BIOSYNTHESIS

Certain *Arabidopsis* mutants of the *transparent testa* (*tt*) phenotype do not make the anthocyanin pigment cyanidin and therefore have no seed coat color. The genes responsible for many of these mutants have now been identified as shown in Table 5.

10

TABLE 5

Enzyme	Abbreviation	Locus	Chromosome
Dihydroflavanol-4-reductase	DFR	<i>tt3</i>	5
Chalcone synthase	CHS	<i>tt4</i>	5
Chalcone isomerase	CHI	<i>tt5</i>	3
Flavanone 3- β -hydroxylase	F3 β H	<i>tt6</i>	3

Over-expression of the maize genes for CHS, CHI and DFR has been shown to complement the *Arabidopsis tt4*, *tt5* and *tt3* mutants, respectively, thereby restoring cyanidin synthesis and seed coat color (Dong *et al.*, *Plant Physiol.* 127:46-57, 2001).
 15 Complementation of these *Arabidopsis* mutants may therefore be employed to demonstrate the function of the inventive polynucleotides encoding enzymes involved in the tannin biosynthetic pathway.

Sense constructs containing a polynucleotide including the coding region of tannin genes isolated from *L. perenne* or *F. arundinacea* LpCHS, LpCHI, LpF3 β H, LpDFR1, FaCHI and FaF3 β H (SEQ ID NO: 157, 55, 161, 159, 56 and 62, respectively) under the control of the CaMV 35S promoter were inserted into a binary vector and used to transform *Agrobacterium tumefaciens* LBA4404 using published methods (*see*, An G, Ebert PR, Mitra A, Ha SB, "Binary Vectors," in Gelvin SB, Schilperoort RA, eds., *Plant Molecular Biology Manual*, Kluwer Academic Publishers: Dordrecht, 1988). The presence and integrity of the
 20 binary vector in *A. tumefaciens* was verified by polymerase chain reaction (PCR) using the primer pairs described in Table 6.

TABLE 6

Gene	SEQ ID NO:	Transparent testa line	Forward Primer SEQ ID NO:	Reverse Primer SEQ ID NO:
LpCHS	157	<i>tt4</i>	211	212
LpCHI	55	<i>tt5</i>	213	214
LpF3 β H	161	<i>tt6</i>	217	218
LpDFR1	159	<i>tt3</i>	215	216
FaCHI	56	<i>tt5</i>	213	214
FaF3 β H	62	<i>tt6</i>	217	218

5 The *A. tumefaciens* containing the sense gene constructs are used to transform *Arabidopsis* by floral dipping (Clough and Bent, *Plant J.* 16:735-743, 1998). Several independent transformed plant lines were established for the sense construct for each of the tannin genes. Specifically, LpDFR1 constructs were transformed into *Arabidopsis tt3* mutants, LpCHS constructs were transformed into *Arabidopsis tt4* mutants, LpCHI and
10 FaCHI constructs were transformed into *Arabidopsis tt5* mutants, and LpF3 β H and FaF3 β H constructs were transformed into *Arabidopsis tt6* mutants. Several independent transformed plant lines were established for the construct for each of the tannin genes. Transformed plants containing the appropriate tannin gene construct were verified using PCR.

15 The presence of cyanidin in the FaCHI transformed plants is demonstrated by a phenotypic change in plant seedling color and by analyzing cyanidin extracts made from transgenic plants grown under stressed conditions (Dong *et al.*, *Plant Physiol.* 127:46-57, 2001). Briefly, cyanidins are extracted from plant tissue with an acid/alcohol solution (HCl/methanol) and water. Chlorophyll is removed by freezing the extracts followed by centrifugation at 4 °C at 20,000 *g* for 20 min. Any remaining chlorophyll is removed through
20 a chloroform extraction. The absorbance at 530 nm is measured for each of the cyanidin extracts. Non-transgenic wild type and control *Arabidopsis* plants are used as controls.

SEQ ID NOS: 1-218 are set out in the attached Sequence Listing. The codes for nucleotide sequences used in the attached Sequence Listing, including the symbol "n," conform to WIPO Standard ST.25 (1998), Appendix 2, Table 1.

5 All references cited herein, including patent references and non-patent publications, are hereby incorporated by reference in their entireties.

While in the foregoing specification this invention has been described in relation to certain preferred embodiments, and many details have been set forth for purposes of illustration, it will be apparent to those skilled in the art that the invention is susceptible to additional embodiments and that certain of the details described herein may be varied
10 considerably without departing from the basic principles of the invention.

Claims

We claim:

1. An isolated polynucleotide comprising a sequence selected from the group consisting of:
 - (a) SEQ ID NO: 1-62 and 125-162;
 - (b) complements of SEQ ID NO: 1-62 and 125-162;
 - (c) reverse complements of SEQ ID NO: 1-62 and 125-162; and
 - (d) reverse sequences of SEQ ID NO: 1-62 and 125-162;
2. An isolated polynucleotide comprising a sequence selected from the group consisting of:
 - (a) sequences having a 99% probability of being functionally or evolutionarily related to a sequence of SEQ ID NO: 1-62 and 125-162;
 - (b) sequences having at least 75% identity to a sequence of SEQ ID NO: 1-62 and 125-162;
 - (c) sequences having at least 90% identity to a sequence of SEQ ID NO: 1-62 and 125-162; and
 - (d) sequences having at least 95% identity to a sequence of SEQ ID NO: 1-62 and 125-162,wherein the polynucleotide encodes a polypeptide having substantially the same functional properties as a polypeptide encoded by SEQ ID NO: 1-62 and 125-162.
3. An isolated oligonucleotide probe or primer comprising at least 10 contiguous residues complementary to 10 contiguous residues of a nucleotide sequence recited in claim 1.
4. A kit comprising a plurality of oligonucleotide probes or primers of claim 3.
5. A genetic construct comprising an isolated polynucleotide of any one of claims 1 and 2.

6. A transgenic cell comprising a construct according to claim 5.
7. A construct comprising, in the 5'-3' direction:
 - (a) a gene promoter sequence;
 - (b) a polynucleotide sequence comprising at least one of the following: (1) a polynucleotide coding for at least a functional portion of a polypeptide encoded by a polynucleotide of any one of claims 1 and 2; and (2) a polynucleotide comprising a non-coding region of a polynucleotide of any one of claims 1 and 2; and
 - (c) a gene termination sequence.
8. The construct of claim 7, wherein the polynucleotide is in a sense orientation.
9. The construct of claim 7, wherein the polynucleotide is in an anti-sense orientation.
10. A transgenic plant cell comprising a construct of claim 7.
11. A plant comprising a transgenic plant cell according to claim 10, or fruit or seeds or progeny thereof.
12. A method for modulating one or more of the lignin composition, fructan composition and tannin composition of a plant, comprising stably incorporating into the genome of the plant at least one polynucleotide of any one of claims 1 and 2.
13. The method of claim 12, wherein the plant is selected from the group consisting of grasses.
14. The method of claim 13, wherein the plant is selected from the group consisting of: *Lolium perenne* and *Festuca arundinacea*.

15. The method of claim 12 comprising stably incorporating into the genome of the plant a construct of claim 7.

16. A method for producing a plant having one or more of altered lignin composition, altered fructan composition and altered tannin composition, comprising:

- (a) transforming a plant cell with a construct of claim 7 to provide a transgenic cell; and
- (b) cultivating the transgenic cell under conditions conducive to regeneration and mature plant growth.

17. A method for modifying the activity of a polypeptide involved in a lignin, fructan or tannin biosynthetic pathway in a plant comprising stably incorporating into the genome of the plant a construct of claim 7.

18. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of: SEQ ID NO: 63-124 and 163-190.

19. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of:

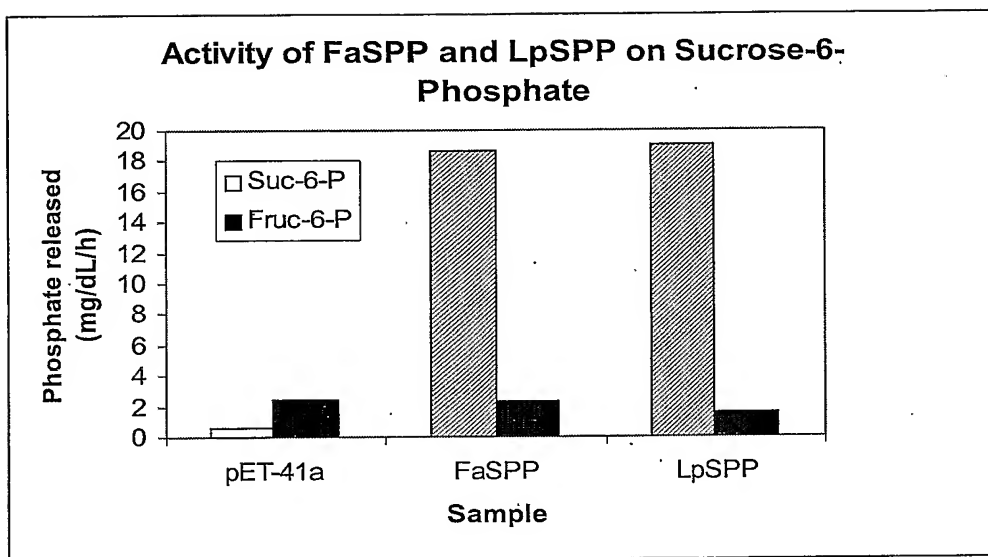
- (a) sequences having at least 75% identity to a sequence of SEQ ID NO: 63-124 and 163-190;
- (b) sequences having at least 90% identity to a sequence of SEQ ID NO: 63-124 and 163-190; and
- (c) sequences having at least 95% identity to a sequence of SEQ ID NO: 63-124 and 163-190

wherein the polypeptide has substantially the same functional properties as a polypeptide of SEQ ID NO: 63-124 and 163-190.

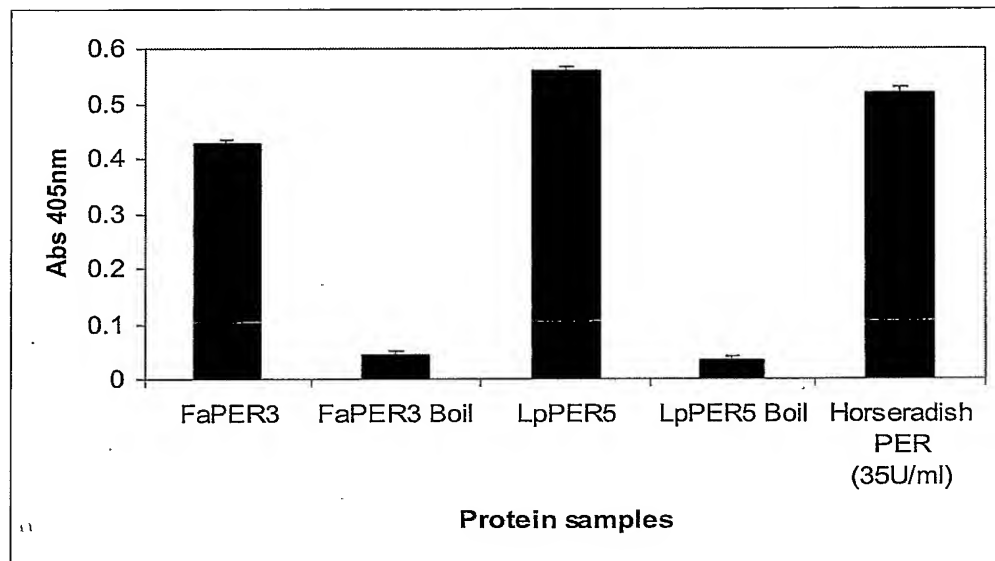
20. An isolated polynucleotide that encodes a polypeptide of claim 18.

21. An isolated polypeptide encoded by a polynucleotide of any one of claims 1 and 2.

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**Figure 1.**

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**Figure 2.**

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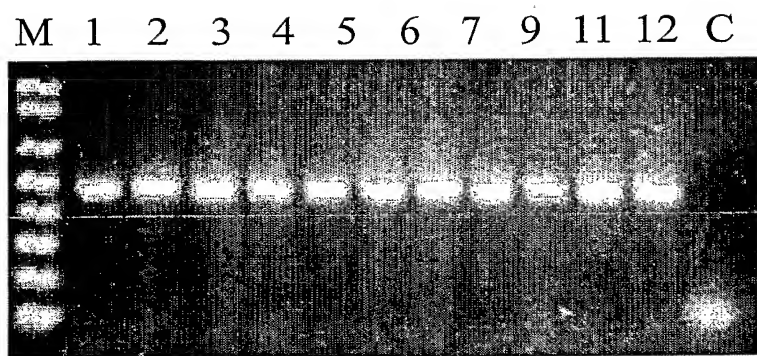


Figure 3.

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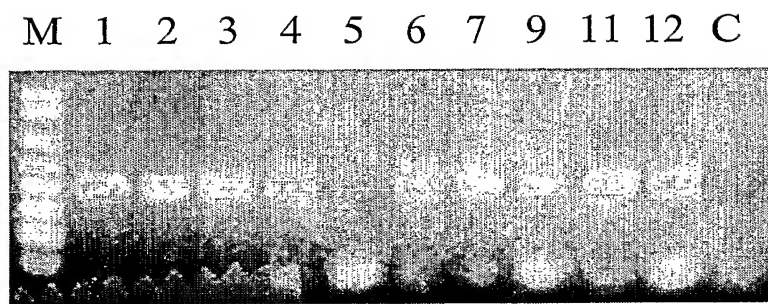


Figure 4.

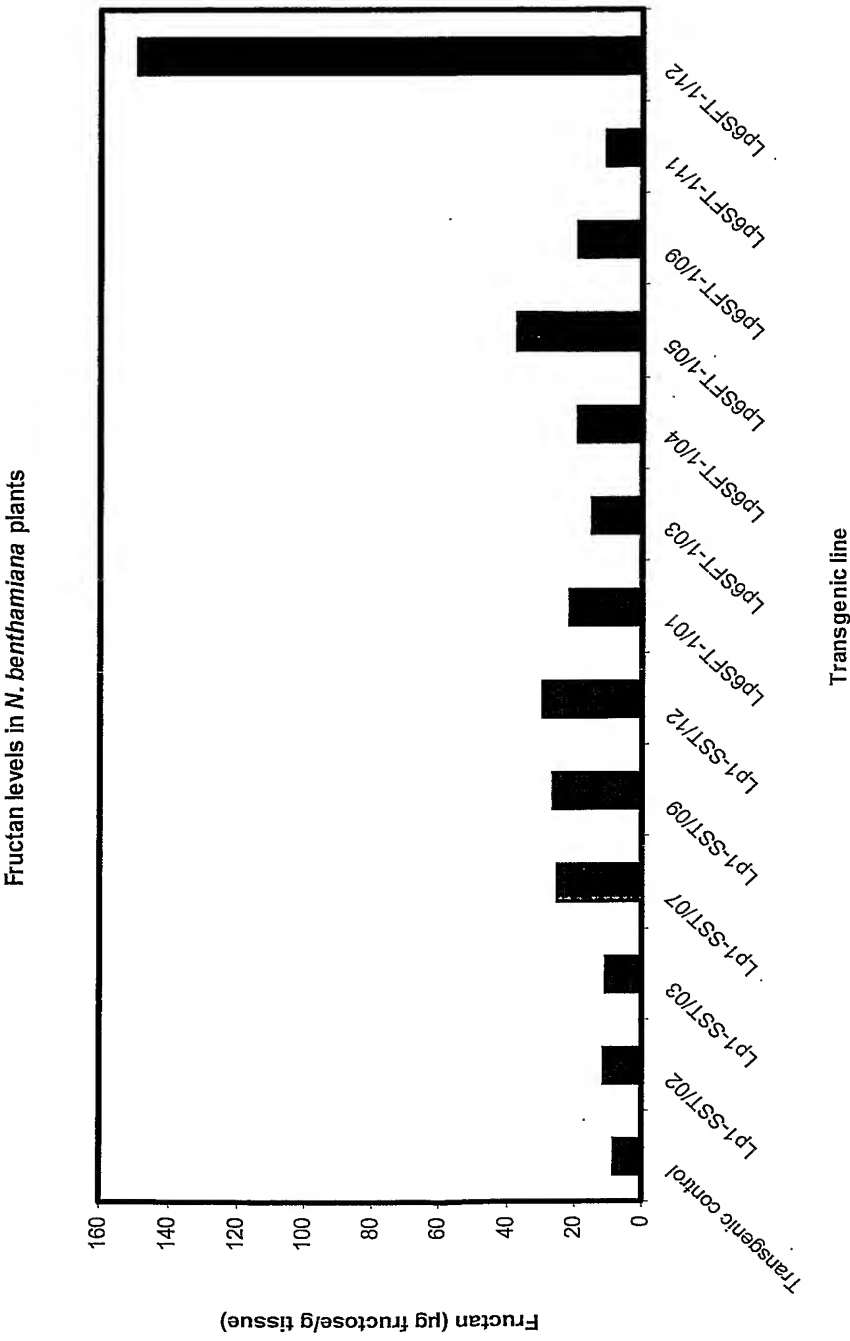
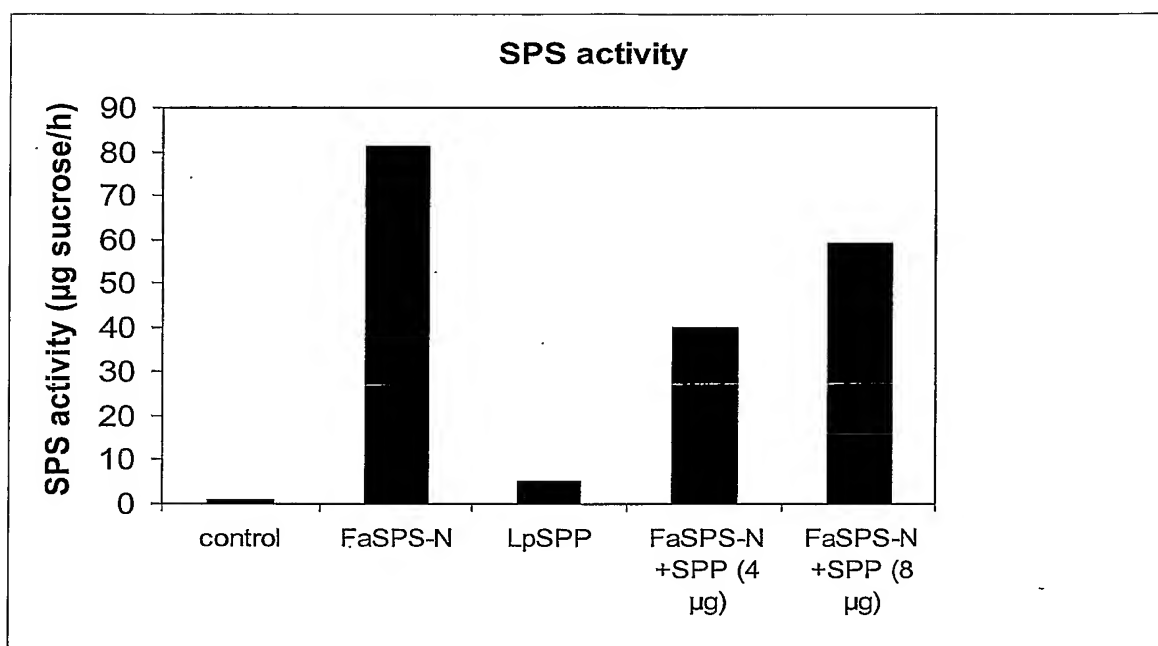
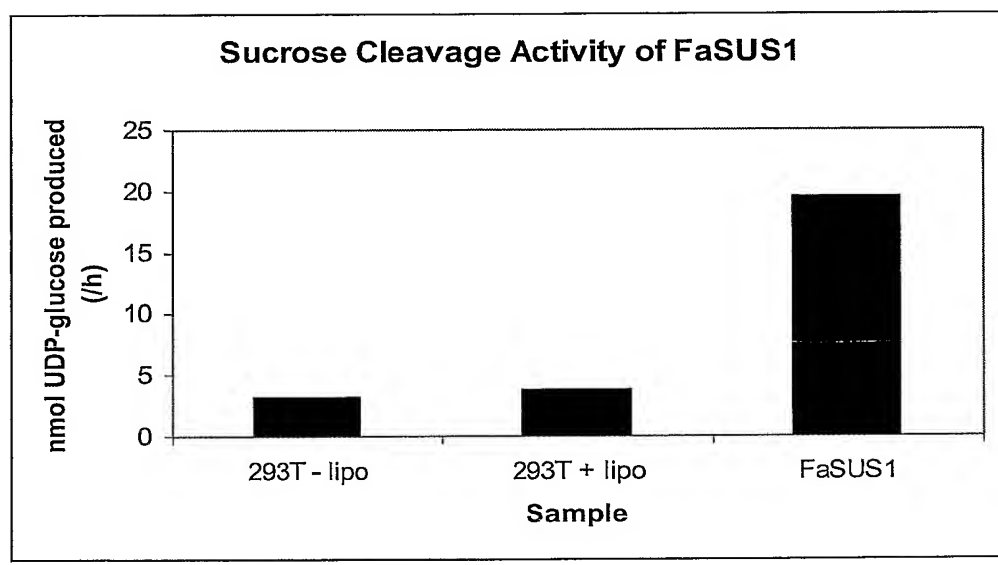


Figure 5.

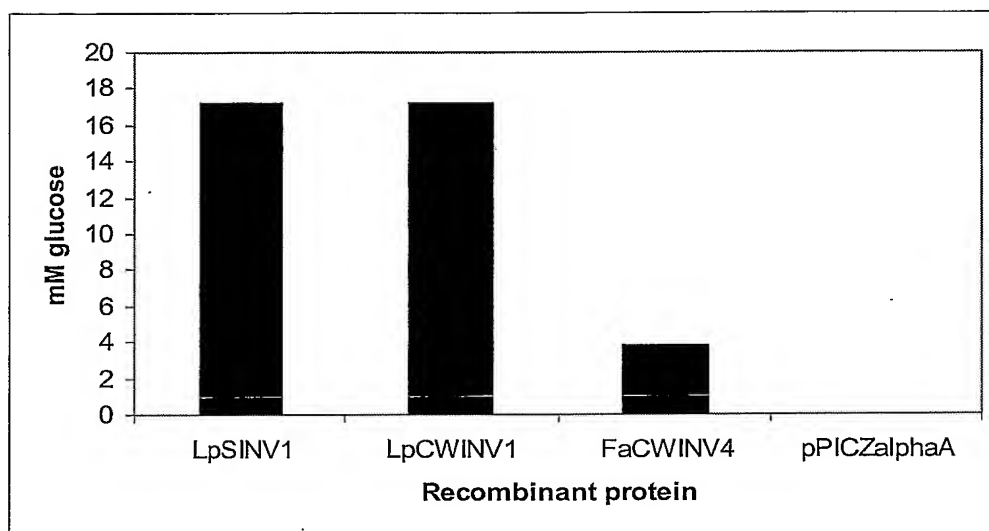
6/8

**Figure 6.**

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**Figure 7.**

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**Figure 8.**

SEQUENCE LISTING

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 Shenk, Michael Andrew
 Norriss, Geoffrey
 Glenn, Matthew
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<212> DNA

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<211> 1778

<212> DNA

<213> Lolium perenne

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<211> 3629

<212> DNA

<213> Festuca arundinacea

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<212> DNA

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<212> DNA

<213> Festuca arundinacea

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<213> Lolium perenne

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<210> 22

<211> 1760

<212> DNA

<213> Lolium perenne

<400> 22

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<210> 23

<211> 2059

<212> DNA

<213> Festuca arundinacea

<400> 23

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<210> 24
<211> 2167
<212> DNA
<213> *Lolium perenne*

<400> 24
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<210> 25
<211> 2138
<212> DNA
<213> *Lolium perenne*

<400> 25
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<210> 26

<211> 1768

<212> DNA

<213> *Lolium perenne*

<400> 26

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<210> 27
 <211> 1855
 <212> DNA
 <213> *Lolium perenne*

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<210> 28
 <211> 2041
 <212> DNA
 <213> *Lolium perenne*

<400> 28
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<210> 29

<211> 1934

<212> DNA

<213> Festuca arundinacea

<400> 29

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<210> 30

<211> 2014

<212> DNA

<213> Lolium perenne

<400> 30

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<210> 31

<211> 2073

<212> DNA

<213> Festuca arundinacea

<400> 31

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<210> 32

<211> 1798

<212> DNA

<213> *Lolium perenne*

<400> 32

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<210> 33

<211> 1775

<212> DNA

<213> *Festuca arundinacea*

<400> 33

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<210> 34

<211> 1323

<212> DNA

<213> *Lolium perenne*

<400> 34

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aaa						1323

<210> 35

<211> 1313

<212> DNA

<213> *Festuca arundinacea*

<400> 35

ggtcccaagc	ccacccaatc	ctcaccagca	tctctctcgc	ccacgcctcc	gatctcctct	60
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ggtaggcgag	gtggtggagg	tcgggcccga	ggtgagcaag	tacagcgctg	gcgacgtggt	360
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<210> 36

<211> 1059

<212> DNA

<213> *Lolium perenne*

<400> 36

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gccagcgggt	ccgagcaggt	caccgcgccac	tccgaggctcg	ggcacaagag	cctgctccag	180
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<210> 37

<211> 1063

<212> DNA

<213> *Festuca arundinacea*

<400> 37

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aatttatatc cagacaaata atattactcc tataaaaaaa aaa 1063

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<210> 38
<211> 1333
<212> DNA
<213> Lolium perenne

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<400> 38
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tgtctctgac cccgcctcac cgccggccgg ttctccgctc cgagctatac gtccgtccga 120
gaacacccgt cccatattaa ctatcaacat gacagtcgtc gaggtcttag ctgccggcga 180
cgccgcgcgc gccgcggtgg cgccggccgc cggaacggg cagaccgtgt gtgtgaccgg 240
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tgtaaaaaaa aaa 1333

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<210> 39
<211> 1237
<212> DNA
<213> Festuca arundinacea

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<400> 39
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<210> 40
<211> 1429
<212> DNA
<213> Festuca arundinacea

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<400> 40
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<210> 41
<211> 1457
<212> DNA
<213> *Lolium perenne*

<400> 41
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<210> 42
<211> 1452
<212> DNA
<213> *Festuca arundinacea*

<400> 42

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<210> 43

<211> 1440

<212> DNA

<213> Lolium perenne

<400> 43

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<210> 44

<211> 2102

<212> DNA

<213> Lolium perenne

<400> 44

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<210> 45

<211> 2051

<212> DNA

<213> Festuca arundinacea

<400> 45

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<210> 46

<211> 2461

<212> DNA

<213> *Lolium perenne*

<400> 46

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<210> 47

<211> 2596

<212> DNA

<213> *Festuca arundinacea*

<400> 47

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<210> 48

<211> 1301

<212> DNA

<213> *Festuca arundinacea*

<400> 48

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<210> 49

<211> 1236

<212> DNA

<213> *Lolium perenne*

<400> 49

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<210> 50

<211> 1205

<212> DNA

<213> *Festuca arundinacea*

<400> 50

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tcgcgggcgt	ggcggcgtct	tgcgctcatg	cacagctgca	cgagaagtcc	tacagttagt	180
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aaaaa						1205

<210> 51
 <211> 1382
 <212> DNA
 <213> *Lolium perenne*

<400> 51
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 ggccgcggcc accaagatca gtgtctccact accgccgctg gccaagggcc tgaacttcga 180
 tttctacaag gccacctgcc cgcaggccga gtccatcgtc tccaacttcc tccgcgacgc 240
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 cgcgtatcc ggccgcgaca cgctcggcat cgcgcactgc acctccttc aggagcgctt 720
 cttcccgag aacgacgtca cctcaacaa gtgggttcgc tcgcagctca ggctcacttg 780
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 ttogaccag ttctgtcttct ccgtcgtcaa gatggggcag atcaacgtgc tcaccggcag 1020
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 gccgtggtcc gtgctcgaga ccgtcaccga ggccgcccag agcttggtgt tgtagatatg 1140
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 tgtagcttta ttagcgagcc gtgtggtaat ggtttgggtc ttgagagcca cagttgatgc 1260
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 aa 1382

<210> 52
 <211> 1261
 <212> DNA
 <213> *Lolium perenne*

<400> 52
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 aaggttctgg gctgtccgtc gggttctaca agaagttgtg tccgaaggcg gagaaggtcg 180
 tccggcgaa tgacaccaag gccttttgaga aggagcctgg caccggggcc gacatcatcc 240
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 ttcatttgg ttcatatggt ggtgagaaat atataacat ttgtttgcgt cataaactgt 1200
 aaagcttaca cagcatgcat aaaagcatct atatcattcc atttgagttg taaaaaaaaa 1260
 a 1261

<210> 53
 <211> 1059
 <212> DNA
 <213> *Lolium perenne*

<400> 53
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 gtgacgacgg cgggtgctgct ggaccaccgc atgggcgctt ctcttctccg gctccacttc 120
 cactgactgct ttgtgcaagg gtgacgacgg tccgttctgc tggatgacac gccgggcttc 180
 accggcgaga agggggccgg gccgaacgcc ggggtcgctgc gcgggtctgga ggtgatcgac 240
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 gataacggct acttctccgg cctcctctcc cgccaggggc tgctccattc cgaccaggcg 720
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 tccatgttaa gatggtggca ttggttttaa aaaaaaaaaa 1059

<210> 54

<211> 1266

<212> DNA

<213> Festuca arundinacea

<400> 54
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 tctggccgcc acggcgggcg cggcgagcgt gtctgcaacg ttctatgaca cgtcgtgccc 180
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 cggcgtcatc gacaacatca agaccagcgt cgagggtatc tgcaagcaga ccgtctcctg 420
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 atgcaaaggc ataaagaatt acttcaatat atacaactac aactaccatt attctcaaaa 1260
 aaaaaa 1266

<210> 55

<211> 1164

<212> DNA

<213> Lolium perenne

<400> 55
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 tcaggctcct ctctctctcc cctggccctg gaggcagtcg gtcggatctg gccggtcgcc 180
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 ccgcgcgtgg cccgtccgcc gggcacagcc cagcgcact tcctcgccgg cgcagggtgtg 420
 cgaggggatgg agctcggcgg caacttcatc aagttcacgg ccatcggcgt gtacctgcag 480
 gccgacgcgg ccgtgtccgc gtcgccacg aagtgggccg ggaaaccgcg cgacgagctt 540
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aaccgctgcc	caagaaaaaa	aaaa				1164

<210> 56

<211> 933

<212> DNA

<213> Festuca arundinacea

<400> 56

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ccgccgggca	cagcccacgc	gcacttcctc	gccggcgcgag	gtgtgcgagg	gatggagctc	180
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<210> 57

<211> 1531

<212> DNA

<213> Lolium perenne

<400> 57

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gccgcgacga	tgaccgtgga	ggaggtgagg	aaggcacagc	gggcggaggg	gccgcgcgacg	180
gtgttgccca	tcggcacggc	gacgcccgtc	aactgtgtct	accaggctga	ctacccggac	240
tactacttca	agatcaccaa	gagcgaccac	ctgcgcgatc	tcaaggagaa	gttcaagagg	300
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gagaacccca	acatgtgcgc	gtacatggcg	ccgtcgtctg	acgcgcgcca	ggacatagtt	420
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ctgctatcca	aagtaatttg	tattgtattc	atgcatacct	ggtttgtatt	tgttggtagg	1440
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<210> 58
 <211> 774
 <212> DNA
 <213> Festuca arundinacea

<400> 58							
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<210> 59
 <211> 1211
 <212> DNA
 <213> Lolium perenne

<400> 59							
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cctcgctcct	aacccccaaa	aggagcttgt	ggtgcccggc	gtggaggcca	cgtccaacgt		360
gctgcgcgac	gccaagggaag	ctgggggagt	gcccgggggt	gtggtgacct	cctccgtctc		420
cggcctcgct	ccctgcccgg	ggtggccggc	cggcgagggt	ctcgacgagc	gctgctggac		480
cgacatcgac	tactgcgaca	agaacggggt	ttggtaccct	gcttcaaagg	cactggcgga		540
gaaggcggga	tggaaagttg	cagaggagaa	tggactggat	gtggtgacgg	tcaatccagg		600
gacggttttt	ggcgagatga	ttccgccaag	gctcaatgcc	agcatggcca	tgttctctcg		660
cttacttgaa	gggtgcaaag	aggagtatgc	agatttcttc	atcggggccag	tgacagtgga		720
agacgttgca	ttagcccata	ttctgctgta	cgagaatccg	tcagcatccg	ggaggcacct		780
ctgcgtggag	cccattctgt	actggagtgt	tttcgcccgc	aaagtgcgag	agctctaccc		840
tgattacaaa	gttccaaaat	tccctgagga	cacacagcct	gggctgggtga	ggcggaaggc		900
ggtgccaaaa	aagctgatgg	cggtgggttt	gcagttcact	cctcttgaga	agatcatcag		960
ggatgccgtg	gagagcctca	agagcagagg	atgcatcgcc	tgatgattgg	atcggttaggc		1020
atgtcacctc	tccgtcgtag	gttcatgatc	atccttggtg	aaaaatgtgt	tgtgttggtg		1080
ccagcccagt	gcctacccag	accatatact	taccagtatg	atttgtgcaa	taacagccgg		1140
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<210> 60
 <211> 1229
 <212> DNA
 <213> Lolium perenne

<400> 60							
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cgaagaaaag	ttggacacct	ttggaaaacta	ccaggtgcaa	atgagaggct	ccaacttgtg		180
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ttccacattg	cgtcgcctgt	ccttgggaaa	tctgattcca	attgcaagga	agcaacactc		300
ggtctgcaa	tcaatggtac	cctcaacgtg	ctaagatcct	gcaagaagag	tcattttctc		360
aaaagggttg	ttctcacatc	ttcatcatcc	gcggtaagga	ttagggatga	aactcagcag		420
ccagaactgt	tatgggatga	aacgacatgg	agctctgtgc	cactctgtga	aaagctacag		480
ctatggtatg	ccctggcaaa	gggtatttgca	gagaaagcag	cattggactt	tgccaaggag		540
aataacattg	accttgtgac	agttcttcca	tcattcgtaa	ttggacccag	tttatcccat		600
gaattgtgca	ctactgcttc	agatatacct	ggcttacttc	aaggtagcac	agacaggttc		660
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gtgtacgaaa	caccggaggc	aactggcaga	tatctgtgca	gctcagtggg	tctggataac	780
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aagaacccct	atggaaagca	ggcataccag	ctagacacat	ccaagctcca	ggggctgggt	900
ctcaagtcca	aaggagtcca	ggagatgttt	aacgactgcg	tcgaatcgct	gaaagatcag	960
ggccatttgc	tggagtgcgc	gttgtgataa	cagagacagc	attgacaagc	catagccaaa	1020
cagcattgac	aagccatagc	caaacacatc	tcaactatgc	ctgaatcatg	tcagttctcg	1080
agtcatagat	tttttttttc	tcttcaaata	attcccatgt	actctcctta	ctataccgaa	1140
catcaattgt	cagcggcaga	ttaaatgtgt	ccatatgtct	tgcaattggt	tcaattagta	1200
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<210> 61

<211> 1439

<212> DNA

<213> *Lolium perenne*

<400> 61

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gccgtccttc	gtgcgggacg	aggacgagcg	gcccagggtg	gcgcacgacc	gcttcagcga	180
cgaggtgccc	gtcatctcgc	tccacggcat	cgacgacgcg	cggaggaccg	agatccggga	240
ccgcgtggcg	gcggcggtcg	aggggtgggg	catcttccag	gtcgtcgacc	acggcgctcg	300
gcgccgcgtc	atcgccgaga	tggccaggct	ctcgcgcgac	ttcttcgcgc	tccccgcga	360
ggacaagctc	cgctacgaca	tgtccggcgg	caagaagggc	ggattcatcg	tctccagcca	420
cctccagggc	gagacggtcc	aggactggcg	ggagatcggt	acctacttct	cgtaccgggt	480
caaggcgcg	gactacggcc	ggtggccgga	caagcccgcg	gggtggcgcg	cgtgtggtgga	540
gcagtacagc	gagcggctca	tggcgctgtc	ctgcaagctg	ctgggggtgc	tgtcggaggc	600
catgggcctg	gagacggagg	ccctgtccaa	ggcgtgcgtg	gacatggacc	agaagggtgg	660
ggtcaacttc	taccccaagt	gccccagcc	cgacctcacc	ctcggcctca	agcgccacac	720
cgaccccggc	accatcaccc	tctcctcca	ggacctcgtc	ggcggactcc	aggccacccg	780
cgacggcggc	aacacctgga	tcaccgtaca	gcccacgcgc	ggcgcatctc	tgtcaaacct	840
cggcgaccac	ggccactact	tgagcaacgg	gagggtttaag	aacgcggacc	accaggcggt	900
ggtgaacggg	gagagcagca	ggctgtccat	cgccacgttc	cagaaccggg	cgcccgaacg	960
caaggtgtgg	ccgctggcgg	tgaggagggg	tgaggacacc	atcctggagg	agcccatcac	1020
cttcaccgag	atgtaccgcc	gcaagatggc	gcgcgacctc	gagctcgcca	agcgcaagaa	1080
gcaggccaag	gccgatcagc	tcaagcagca	gctgcagcag	gaggccgcgc	ccgccgccgc	1140
gcccaccaag	ccactcaacc	agattcttgc	ctagattcca	tgccgattca	ttcatgcgtg	1200
atatatagta	ctatgtacta	tatcgtatta	aaataagtaa	ttatctctat	ctactcattt	1260
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ctggacctgt	aataacatgt	agcatgtcct	acgtggaacc	gatcagctga	ttggagctgt	1380
cacatgagtt	tgctgtgtgc	agaaattgaa	cgcattcggt	actgctttca	aaaaaaaaa	1439

<210> 62

<211> 1320

<212> DNA

<213> *Festuca arundinacea*

<400> 62

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gcgccgttcc	tgccgacggc	ggcgacgggc	gaggccacgc	tgccggccgtc	cttcgtgcgg	180
gacgaggacg	agcgacccaa	ggtggcgcac	gaccgcttca	gcgacgagg	gccggtcatc	240
tcgctccacg	gcatcgatga	tggcggcgcg	cggaggggccg	agatccggga	ccgctggcgg	300
gcggcggtcg	aagggtgggg	cgtcttccag	gtcgtcgacc	acggcgctcg	cgccgccctc	360
gtcgccgaga	tggccaggct	ctcccgcgag	ttcttcgcac	tccccgccga	ggacaagctc	420
cgctacgaca	tgtccggcgg	caagaaaggt	ggattcatcg	tctccagcca	cctccagggc	480
gagacggtcc	aggactggcg	ggagatcggt	acctacttct	cgtaccgggt	gaaggcgccg	540
gactacgggc	ggtggccgga	gaagcctgcg	gggtggcgcg	cgtgtggtgga	gcagtacagc	600
gagcggctca	tggcgctgtc	gtgcaagctg	ctgggggtgc	tgtcggaaagc	catgggcctg	660
gagacggagg	ccctgtccaa	ggcgtgcgtg	gacatggacc	agaagggtgg	ggtcaacttc	720
taccccaagt	gccccagcc	cgacctcacc	ctcggtctca	agcgccacac	cgaccccggc	780
accatcaccc	tctcctcca	ggacctcgtc	ggcggactcc	aggccactcg	cgacggcgcc	840
aacacctgga	taccggtgca	gcccgtcccc	ggcgacttcc	tcgtcaacct	cggcgaccac	900
ggccactact	tgagcaacgg	gagggtttaag	aacgcggacc	accaggcggt	ggtcaacggg	960
gagagcagca	ggctgtccat	cgccacgttc	cagaaccggg	cgccagaagc	gaaggtgtgg	1020
ccgctggcgg	taaggagggg	ggaggacacc	atactggagg	agcccatcac	cttcaccgag	1080
atgtaccgcc	gcaagatggc	gtgcgacctc	gagctcgcca	agcgcaagaa	gcaggccaag	1140

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gccgaccagc tcaagcagca gctgcagcag gagcagcagg aggcgggtggc cgccgccgcg 1200
cccaagcccg ccaccaccaa gcccctcaac cagattcttg cctagattcc atgtatatgt 1260
atatcgtatt aaaataagaa attatctata tatatatata tatatataaa aaaaaaaaaa 1320

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<210> 63
<211> 654
<212> PRT
<213> Lolium perenne

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<400> 63
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Tyr Ala Tyr Ala Pro Leu Pro Ser Ser Asp Asp Ala Arg Glu Asn
20     25     30
Arg Ser Ser Gly Gly Val Arg Trp Arg Ala Cys Ala Val Val Leu Ala
35     40     45
Asp Ser Ala Leu Ala Val Val Val Val Gly Leu Leu Ala Gly Gly
50     55     60
Arg Val Asp Arg Val Pro Ala Gly Ala Asp Val Ala Ser Ala Thr Val
65     70     75     80
Pro Ala Val Pro Met Glu Phe Pro Arg Ser Arg Gly Lys Asp Leu Gly
85     90     95
Val Ser Glu Lys Ser Ser Gly Ala Tyr Ser Ala Asp Gly Gly Phe Pro
100    105    110
Trp Ser Asn Ala Met Leu Gln Trp Gln Arg Thr Gly Phe His Phe Gln
115    120    125
Pro Glu Gln His Tyr Met Asn Asp Pro Asn Gly Pro Val Tyr Tyr Gly
130    135    140
Gly Trp Tyr His Leu Phe Tyr Gln His Asn Pro Lys Gly Asp Ser Trp
145    150    155    160
Gly Asn Ile Ala Trp Ala His Ala Val Ser Lys Asp Met Val Asn Trp
165    170    175
Arg His Leu Pro Leu Ala Met Val Pro Asp Gln Trp Tyr Asp Ser Asn
180    185    190
Gly Val Leu Thr Gly Ser Ile Thr Val Leu Pro Asp Gly Gln Val Ile
195    200    205
Leu Leu Tyr Thr Gly Asn Thr Asp Thr Leu Ala Gln Val Gln Cys Leu
210    215    220
Ala Thr Pro Ala Asp Pro Ser Asp Pro Leu Leu Arg Glu Trp Ile Lys
225    230    235    240
His Pro Ala Asn Pro Ile Leu Phe Pro Pro Gly Ile Gly Leu Lys
245    250    255
Asp Phe Arg Asp Pro Leu Thr Ala Trp Phe Asp His Ser Asp His Thr
260    265    270
Trp Arg Thr Val Ile Gly Ser Lys Asp Asp Asp Gly His Ala Gly Ile
275    280    285
Ile Leu Ser Tyr Lys Thr Lys Asp Phe Val Asn Tyr Glu Leu Met Pro
290    295    300
Gly Asn Met His Arg Gly Pro Asp Gly Thr Gly Met Tyr Glu Cys Ile
305    310    315    320
Asp Leu Tyr Pro Val Gly Gly Asn Ser Ser Glu Met Leu Gly Gly Asp
325    330    335
Asp Ser Pro Asp Val Leu Phe Val Leu Lys Glu Ser Ser Asp Asp Glu
340    345    350
Arg His Asp Tyr Tyr Ala Leu Gly Arg Phe Asp Ala Val Ala Asn Val
355    360    365
Trp Thr Pro Ile Asp Arg Asp Leu Asp Leu Gly Ile Gly Leu Arg Tyr
370    375    380
Asp Trp Gly Lys Tyr Tyr Ala Ser Lys Ser Phe Tyr Asp Gln Lys Lys
385    390    395    400
Asn Arg Arg Ile Val Trp Ala Tyr Ile Gly Glu Thr Asp Ser Glu Gln
405    410    415
Ala Asp Ile Thr Lys Gly Trp Ala Asn Leu Met Thr Ile Pro Arg Thr
420    425    430
Val Glu Leu Asp Arg Lys Thr Arg Thr Asn Leu Ile Gln Trp Pro Val
435    440    445

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Glu Glu Val Asp Thr Leu Arg Arg Asn Ser Thr Asp Leu Gly Arg Ile
 450 455 460
 Thr Val Asn Ala Gly Ser Val Ile Arg Leu Pro Leu His Gln Gly Ala
 465 470 475 480
 Gln Leu Asp Ile Glu Ala Ser Phe Gln Leu Asn Ser Ser Asp Val Asp
 485 490 495
 Ala Ile Asn Glu Ala Asp Val Gly Tyr Asn Cys Ser Thr Ser Gly Ala
 500 505 510
 Ala Val Arg Gly Ala Leu Gly Pro Phe Gly Leu Leu Val Leu Ala Asn
 515 520 525
 Gly Arg Thr Glu Gln Thr Ala Val Tyr Phe Tyr Val Ser Lys Gly Val
 530 535 540
 Asp Gly Gly Leu Gln Thr His Phe Cys His Asp Glu Ser Arg Ser Thr
 545 550 555 560
 Arg Ala Lys Asp Val Val Asn Arg Met Ile Gly Ser Ile Val Pro Val
 565 570 575
 Leu Asp Gly Glu Thr Phe Ser Val Arg Val Leu Val Asp His Ser Ile
 580 585 590
 Val Gln Ser Phe Ala Met Gly Gly Arg Ile Thr Ala Thr Ser Arg Ala
 595 600 605
 Tyr Pro Thr Glu Thr Ile Tyr Ala Ala Ala Gly Val Tyr Leu Phe Asn
 610 615 620
 Asn Ala Thr Gly Ala Thr Val Thr Ala Glu Arg Leu Val Val His Glu
 625 630 635 640
 Met Ala Ser Ala Asp Asn His Ile Phe Thr Asn Asp Asp Leu
 645 650

<210> 64

<211> 648

<212> PRT

<213> Festuca arundinacea

<400> 64

Met Glu Ser Ser Ala Val Val Pro Gly Thr Thr Ala Arg Leu Leu Pro
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 Tyr Ala Tyr Ala Pro Leu Pro Ser Ser Ala Asp Asp Ala Arg Glu Asn
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 Gln Gly Ser Asp Gly Val Arg Trp Arg Ala Cys Ala Ala Val Leu Ala
 35 40 45
 Ala Ser Ala Leu Ala Val Leu Val Val Val Gly Leu Leu Ala Gly Gly
 50 55 60
 Arg Val Asp Arg Pro Gly Pro Ala Ala Val Pro Ala Val Pro Thr Glu
 65 70 75 80
 Ile Pro Arg Ser Arg Gly Lys Asp Phe Gly Val Ser Glu Lys Ser Ser
 85 90 95
 Gly Ala Tyr Ser Ala Asp Gly Gly Phe Pro Trp Ser Asn Ala Met Leu
 100 105 110
 Gln Trp Gln Arg Thr Gly Phe His Phe Gln Pro Glu Gln His Tyr Met
 115 120 125
 Asn Asp Pro Asn Gly Pro Val Tyr Tyr Gly Gly Trp Tyr His Leu Phe
 130 135 140
 Tyr Gln Tyr Asn Pro Lys Gly Asp Ser Trp Gly Asn Ile Ala Trp Ala
 145 150 155 160
 His Ala Val Ser Lys Asp Met Val Asn Trp Arg His Leu Pro Leu Ala
 165 170 175
 Met Val Pro Asp Gln Trp Tyr Asp Ser Asn Gly Val Leu Thr Gly Ser
 180 185 190
 Ile Thr Val Leu Pro Asp Gly Arg Val Ile Leu Leu Tyr Thr Gly Asn
 195 200 205
 Thr Asp Thr Leu Ala Gln Val Gln Cys Leu Ala Glu Pro Ala Asp Pro
 210 215 220
 Ser Asp Pro Leu Leu Arg Glu Trp Ile Lys His Pro Ala Asn Pro Ile
 225 230 235 240
 Leu Phe Pro Pro Gly Ile Gly Leu Lys Asp Phe Arg Asp Pro Leu
 245 250 255
 Thr Asp Trp Phe Asp His Ser Asp Asp Thr Trp Arg Thr Val Ile Gly

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                260                265                270
Ser Lys Asp Asp Gly His Ala Gly Ile Ile Leu Ser Tyr Lys Thr
      275                280                285
Lys Asp Phe Val Asn Tyr Glu Leu Met Pro Gly Asn Met His Arg Gly
      290                295                300
Pro Asp Gly Thr Gly Met Tyr Glu Cys Ile Asp Leu Tyr Pro Val Gly
305                310                315                320
Gly Asn Ser Ser Glu Met Leu Gly Gly Asp Asp Ser Pro Asp Val Leu
      325                330                335
Phe Val Leu Lys Glu Ser Ser Asp Asp Glu Arg His Asp Tyr Tyr Ala
      340                345                350
Leu Gly Arg Phe Asp Ala Ala Ala Asn Ile Trp Thr Pro Ile Asp Gln
      355                360                365
Glu Leu Asp Leu Gly Ile Gly Leu Arg Tyr Asp Trp Gly Lys Tyr Tyr
      370                375                380
Ala Ser Lys Ser Phe Tyr Asp Gln Arg Lys Asn Arg Arg Val Val Trp
385                390                395                400
Ala Tyr Ile Gly Glu Thr Asp Ser Glu Gln Ala Asp Ile Thr Lys Gly
      405                410                415
Trp Ala Asn Leu Met Thr Ile Pro Arg Thr Val Glu Leu Asp Lys Lys
      420                425                430
Thr Arg Thr Asn Leu Ile Gln Trp Pro Val Glu Glu Val Asp Thr Leu
      435                440                445
Arg Arg Asn Ser Thr Asp Leu Gly Arg Ile Thr Val Asn Ala Gly Ser
      450                455                460
Val Ile Arg Leu Pro Leu His Gln Gly Ala Gln Leu Asp Ile Glu Ala
465                470                475                480
Ser Phe Gln Leu Asn Ser Ser Asp Val Asp Ala Leu Asn Glu Ala Asp
      485                490                495
Val Gly Tyr Asn Cys Ser Thr Ser Gly Ala Ala Val Arg Gly Ala Leu
      500                505                510
Gly Pro Phe Gly Leu Leu Val Leu Ala Asn Gly Arg Thr Glu Gln Thr
      515                520                525
Ala Val Tyr Phe Tyr Val Ser Lys Gly Val Asp Gly Ala Leu Gln Thr
      530                535                540
His Phe Cys His Asp Glu Ser Arg Ser Thr Arg Ala Lys Asp Val Val
545                550                555                560
Asn Arg Met Ile Gly Ser Ile Val Pro Val Leu Asp Gly Glu Thr Phe
      565                570                575
Ser Val Arg Val Leu Leu Asp His Ser Ile Val Gln Ser Phe Ala Met
      580                585                590
Gly Gly Arg Ile Thr Ala Thr Ser Arg Ala Tyr Pro Thr Glu Ala Ile
      595                600                605
Tyr Ala Ala Ala Gly Val Tyr Val Phe Asn Asn Ala Thr Gly Ala Thr
      610                615                620
Val Thr Ala Glu Arg Leu Val Val Tyr Glu Met Ala Ser Ala Asp Asn
625                630                635                640
His Ile Phe Arg Asn Asp Asp Leu
      645

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<210> 65

<211> 620

<212> PRT

<213> Festuca arundinacea

<400> 65

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Met Glu Ser Arg Ala Phe Pro Asn Ala Ala Tyr Ala Pro Leu Leu Pro
 1                5                10                15
Pro Thr Ala Asp Asp Ala Thr Leu Gly Lys Gln Asp Arg Pro Gly Val
      20                25                30
Gly Trp Arg Gly Phe Leu Thr Val Leu Ala Ala Ser Gly Val Val Val
      35                40                45
Leu Leu Val Ala Ala Thr Met Leu Ala Gly Ser Arg Met Gly Gln Ala
      50                55                60
Gly Asp Thr Asp Glu Asp Gly Ala Gly Gly Phe Pro Trp Ser Asn Glu
65                70                75                80

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Met	Leu	Gln	Trp	Gln	Arg	Ala	Gly	Phe	His	Tyr	Gln	Pro	Glu	Gly	His	
				85					90					95		
Phe	Met	Ser	Asp	Pro	Asp	Gly	Pro	Val	Tyr	Tyr	Arg	Gly	Tyr	Tyr	His	
			100					105					110			
Leu	Phe	Phe	Gln	Tyr	Asn	Arg	Arg	Gly	Val	Ala	Trp	Asp	Asp	Tyr	Ile	
		115					120					125				
Glu	Trp	Gly	His	Val	Val	Ser	Gln	Asp	Leu	Val	His	Trp	Arg	Pro	Leu	
	130					135					140					
Pro	Leu	Ala	Leu	Arg	Pro	Asp	His	Trp	Tyr	Asp	Lys	Lys	Gly	Val	Leu	
145					150					155					160	
Ser	Gly	Thr	Ile	Thr	Val	Leu	His	Asn	Gly	Thr	Leu	Val	Leu	Leu	Tyr	
				165					170					175		
Thr	Gly	Val	Thr	Glu	Asp	Pro	Met	Ala	Glu	Ser	Gln	Cys	Ile	Ala	Val	
			180					185					190			
Pro	Thr	Asp	Pro	Asn	Asp	Pro	Leu	Leu	Arg	His	Trp	Thr	Lys	His	Pro	
		195					200					205				
Ala	Asn	Pro	Val	Leu	Ala	His	Pro	Gln	Gly	Val	Gln	Gly	Met	Asp	Phe	
	210					215					220					
Arg	Asp	Pro	Thr	Ser	Ala	Trp	Phe	Asp	Lys	Ser	Asp	Ala	Thr	Trp	Arg	
225					230				235						240	
Ile	Leu	Ile	Gly	Ser	Lys	Asp	Asp	Asp	Asn	Gly	Ser	His	Ala	Gly	Ile	
				245				250						255		
Ala	Phe	Ile	Phe	Lys	Thr	Lys	Asp	Phe	Leu	Ser	Phe	Glu	Arg	Val	Pro	
			260					265					270			
Gly	Ile	Val	His	Arg	Val	Glu	Gly	Thr	Gly	Met	Trp	Glu	Cys	Ile	Asp	
		275					280					285				
Phe	Tyr	Pro	Val	Gly	Gly	Gly	His	Asn	Ser	Ser	Ser	Glu	Glu	Leu	Tyr	
	290					295					300					
Val	Ile	Lys	Ala	Ser	Met	Asp	Asp	Glu	Arg	His	Asp	Tyr	Tyr	Ser	Leu	
305					310					315					320	
Gly	Arg	Tyr	Asp	Ala	Ala	Ala	Asn	Thr	Trp	Thr	Pro	Leu	Asp	Ala	Glu	
				325					330					335		
Leu	Asp	Leu	Gly	Ile	Gly	Leu	Arg	Tyr	Asp	Trp	Gly	Lys	Leu	Tyr	Ala	
			340					345					350			
Ala	Thr	Ser	Phe	Tyr	Asp	Pro	Leu	Lys	Gln	Arg	Arg	Ile	Met	Leu	Gly	
		355					360					365				
Tyr	Val	Gly	Glu	Thr	Asp	Ser	Ala	Arg	Ala	Asp	Val	Ala	Lys	Gly	Trp	
	370					375					380					
Ala	Ser	Leu	Gln	Ser	Ile	Pro	Arg	Thr	Val	Thr	Leu	Asp	Glu	Lys	Thr	
385					390					395					400	
Arg	Thr	Asn	Leu	Leu	Leu	Trp	Pro	Val	Glu	Glu	Val	Glu	Ala	Leu	Arg	
				405					410					415		
Tyr	Asn	Ser	Thr	Asp	Leu	Ser	Gly	Ile	Thr	Val	Asp	Asn	Gly	Ser	Val	
			420					425					430			
Phe	His	Leu	Pro	Leu	His	Gln	Ala	Thr	His	Leu	Asp	Ile	Glu	Ala	Ser	
		435					440					445				
Phe	Arg	Leu	Asp	Ala	Ser	Asp	Val	Ala	Ala	Ile	Asn	Glu	Ala	Asp	Val	
	450					455					460					
Gly	Tyr	Asn	Cys	Ser	Ser	Ser	Gly	Gly	Ala	Ala	Ala	Arg	Gly	Ala	Ile	
465					470				475					480		
Gly	Pro	Phe	Gly	Leu	Leu	Val	His	Ala	Ala	Gly	Asp	Leu	Arg	Gly	Glu	
				485					490					495		
Gln	Thr	Ala	Val	Tyr	Phe	Tyr	Val	Ser	Arg	Ala	Leu	Asp	Gly	Thr	Leu	
			500					505					510			
Arg	Thr	Ser	Phe	Cys	Asn	Asp	Glu	Thr	Arg	Ser	Ser	Arg	Ala	Arg	Asp	
		515					520					525				
Val	Thr	Lys	Arg	Val	Val	Gly	Ser	Thr	Val	Pro	Val	Leu	His	Gly	Glu	
						535					540					
Ala	Leu	Ser	Met	Arg	Val	Leu	Val	Asp	His	Ser	Ile	Val	Gln	Ser	Phe	
545					550					555					560	
Ala	Met	Gly	Gly	Arg	Val	Thr	Ala	Thr	Ser	Arg	Val	Tyr	Pro	Thr	Glu	
				565					570					575		
Ala	Ile	Tyr	Ala	Arg	Ala	Gly	Val	Tyr	Leu	Phe	Asn	Asn	Ala	Thr	Gly	
			580					585					590			
Ala	Ser	Val	Thr	Ala	Glu	Arg	Leu	Ile	Val	His	Glu	Met	Ala	Ser	Ala	
			595				600					605				

Val Tyr Asp Glu Thr Leu Ile Met Val Glu Asp Ser
 610 615 620

<210> 66

<211> 623 .

<212> PRT

<213> Lolium perenne

<400> 66

Met Glu Ser Arg Ala Phe Pro Ser Ala Ala Tyr Ala Pro Leu Leu Pro
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 20 25 30
 Gly Trp Arg Gly Phe Leu Thr Val Leu Ala Ala Cys Gly Val Val Val
 35 40 45
 Leu Leu Val Gly Ala Thr Leu Ala Gly Ser Arg Met Gly Gln Ala
 50 55 60
 Gly Asp Gly Glu Gly Asn Thr Asp Glu Asp Gly Ala Gly Gly Phe Pro
 65 70 75 80
 Trp Ser Asn Glu Met Leu Gln Trp Gln Arg Ala Gly Phe His Tyr Gln
 85 90 95
 Pro Glu Gly His Phe Met Ser Asp Pro Asn Gly Pro Val Tyr Tyr Arg
 100 105 110
 Gly Tyr Tyr His Leu Phe Phe Gln Tyr Asn Arg Arg Gly Val Ala Trp
 115 120 125
 Asp Asp Tyr Ile Glu Trp Gly His Val Val Ser Gln Asp Leu Val His
 130 135 140
 Trp Arg Pro Leu Pro Leu Ala Met Arg Pro Asp His Trp Tyr Asp Lys
 145 150 155 160
 Lys Gly Val Leu Ser Gly Thr Ile Thr Val Leu His Asn Gly Thr Leu
 165 170 175
 Val Leu Leu Tyr Thr Gly Val Thr Glu Asp Pro Met Ala Glu Ser Gln
 180 185 190
 Cys Ile Ala Val Pro Thr Asp Pro Asn Asp Pro Leu Leu Arg His Trp
 195 200 205
 Thr Lys His Pro Ala Asn Pro Val Leu Ala His Pro Gln Gly Val Gln
 210 215 220
 Gly Met Asp Phe Arg Asp Pro Thr Ser Ala Trp Trp Asp Lys Ser Asp
 225 230 235 240
 Ala Thr Trp Arg Ile Leu Ile Gly Ser Lys Asp Asp Asp Asn Gly Ser
 245 250 255
 His Ala Gly Ile Ala Phe Ile Phe Lys Thr Lys Asp Phe Leu Ser Phe
 260 265 270
 Glu Arg Val Pro Gly Ile Val His Arg Val Glu Gly Thr Gly Met Trp
 275 280 285
 Glu Cys Ile Asp Phe Tyr Pro Val Gly Gly Gly His Asn Ser Ser Ser
 290 295 300
 Glu Glu Leu Tyr Val Ile Lys Ala Ser Met Asp Asp Glu Arg His Asp
 305 310 315 320
 Tyr Tyr Ser Leu Gly Arg Tyr Asp Ala Ala Asn Thr Trp Thr Pro
 325 330 335
 Leu Asp Ala Glu Leu Asp Leu Gly Ile Gly Leu Arg Tyr Asp Trp Gly
 340 345 350
 Lys Leu Tyr Ala Ser Thr Ser Phe Tyr Asp Pro Val Lys Gln Arg Arg
 355 360 365
 Ile Met Leu Gly Tyr Val Gly Glu Val Asp Ser Ala Arg Ala Asp Val
 370 375 380
 Ala Lys Gly Trp Ala Ser Leu Gln Ser Ile Pro Arg Thr Val Ala Leu
 385 390 395 400
 Asp Glu Lys Thr Arg Thr Asn Leu Leu Leu Trp Pro Val Glu Glu Val
 405 410 415
 Glu Ala Leu Arg Tyr Asn Ser Thr Asp Leu Ser Gly Ile Thr Ile Asp
 420 425 430
 Asn Gly Ser Val Phe His Leu Pro Leu His Gln Thr Thr Gln Leu Asp
 435 440 445

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Ile Glu Ala Ser Phe Arg Leu Asp Ala Ser Asp Val Ala Ala Ile Asn
  450          455          460
Glu Ala Asp Val Gly Tyr Asn Cys Ser Ser Ser Gly Gly Ala Ala Ala
465          470          475          480
Arg Gly Ala Leu Gly Pro Phe Gly Leu Leu Val His Ala Ala Gly Asp
          485          490          495
Leu Arg Gly Glu Gln Thr Ala Val Tyr Phe Tyr Val Ser Arg Ala Leu
          500          505          510
Asp Gly Thr Leu Arg Thr Ser Phe Cys Asn Asp Glu Thr Arg Ser Ser
          515          520          525
Arg Ala Arg Asp Val Thr Lys Arg Val Val Gly Ser Thr Val Pro Val
          530          535          540
Leu Asp Gly Glu Ala Leu Ser Met Arg Val Leu Val Asp His Ser Ile
545          550          555          560
Val Gln Ser Phe Ala Met Gly Gly Arg Thr Thr Ala Thr Ser Arg Val
          565          570          575
Tyr Pro Thr Glu Ala Ile Tyr Ala Arg Ala Gly Val Tyr Leu Phe Asn
          580          585          590
Asn Ala Thr Gly Ala Gly Val Thr Ala Glu Arg Leu Ile Val His Glu
          595          600          605
Met Ala Ser Ala Val Tyr Asp Glu Thr Leu Met Val Glu Asp Ser
          610          615          620

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<210> 67

<211> 623

<212> PRT

<213> Festuca arundinacea

<400> 67

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Met Glu Ser Arg Ala Phe Pro Ser Ala Ala Tyr Ala Pro Leu Leu Pro
  1          5          10          15
Pro Thr Ala Asp Asp Ala Thr Leu Gly Lys Gln Asp Arg Pro Gly Val
          20          25          30
Gly Trp Arg Gly Phe Leu Thr Val Leu Ala Ala Ser Gly Val Val Val
          35          40          45
Leu Leu Val Ala Ala Ser Leu Leu Ala Gly Ser Arg Met Gly Gln Ala
          50          55          60
Gly Asp Gly Glu Gly Asn Thr Asp Glu Asp Gly Ala Gly Gly Phe Pro
65          70          75          80
Trp Ser Asn Glu Met Leu Gln Trp Gln Arg Ala Gly Phe His Tyr Gln
          85          90          95
Pro Glu Gly His Phe Met Ser Asp Pro Asp Gly Pro Val Tyr Tyr Arg
          100          105          110
Gly Tyr Tyr His Leu Phe Phe Gln Tyr Asn Arg Arg Gly Val Ala Trp
          115          120          125
Asp Asp Tyr Ile Glu Trp Gly His Val Val Ser Gln Asp Leu Val His
          130          135          140
Trp Arg Pro Leu Pro Val Ala Met Arg Pro Asp His Trp Tyr Asp Lys
145          150          155          160
Lys Gly Val Leu Ser Gly Thr Ile Thr Val Leu His Asn Gly Thr Leu
          165          170          175
Val Leu Leu Tyr Thr Gly Val Thr Glu Asp Pro Met Ala Glu Ser Gln
          180          185          190
Cys Ile Ala Val Pro Thr Asp Pro Asn Asn Pro Leu Leu Arg His Trp
          195          200          205
Thr Lys His Pro Ala Asn Pro Val Leu Ala His Pro Gln Gly Val Gln
          210          215          220
Gly Met Asp Phe Arg Asp Pro Thr Ser Ala Trp Phe Asp Lys Ser Asp
225          230          235          240
Ala Thr Trp Arg Ile Leu Ile Gly Ser Lys Asp Asp Asp Asn Gly Ser
          245          250          255
His Ala Gly Ile Ala Phe Ile Phe Lys Thr Lys Asp Phe Leu Ser Phe
          260          265          270
Glu Arg Val Pro Gly Ile Val His Arg Val Glu Gly Thr Gly Met Trp
          275          280          285

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Glu Cys Ile Asp Phe Tyr Pro Val Gly Gly Gly His Asn Ser Ser Ser
 290 295 300
 Glu Glu Leu Tyr Val Ile Lys Ala Ser Met Asp Asp Glu Arg His Asp
 305 310 315 320
 Tyr Tyr Ser Leu Gly Arg Tyr Asp Ala Ala Ala Asn Thr Trp Thr Pro
 325 330 335
 Leu Asp Ala Glu Leu Asp Leu Gly Ile Gly Leu Arg Tyr Asp Trp Gly
 340 345 350
 Lys Leu Tyr Ala Ala Thr Ser Phe Tyr Asp Pro Leu Lys Gln Arg Arg
 355 360 365
 Ile Met Leu Gly Tyr Val Gly Glu Thr Asp Ser Ala Arg Ala Asp Val
 370 375 380
 Ala Lys Gly Trp Ala Ser Leu Gln Ser Ile Pro Arg Thr Val Thr Leu
 385 390 395 400
 Asp Glu Lys Thr Arg Thr Asn Leu Leu Leu Trp Pro Val Glu Glu Val
 405 410 415
 Glu Ala Leu Arg Tyr Asn Ser Thr Asp Leu Ser Gly Ile Thr Ile Asp
 420 425 430
 Asn Gly Ser Val Phe His Leu Pro Leu His Gln Ala Thr Gln Leu Asp
 435 440 445
 Ile Glu Ala Ser Phe Arg Leu Asp Ala Ser Asp Val Ala Ala Ile Asn
 450 455 460
 Glu Ala Asp Val Gly Tyr Asn Cys Ser Ser Ser Gly Gly Ala Ala Ala
 465 470 475 480
 Arg Gly Ala Ile Gly Pro Phe Gly Leu Leu Val His Ala Ala Gly Asp
 485 490 495
 Leu Arg Gly Glu Gln Thr Ala Val Tyr Phe Tyr Val Ser Arg Ala Leu
 500 505 510
 Asp Gly Thr Leu Arg Thr Ser Phe Cys Asn Asp Glu Thr Arg Ser Ser
 515 520 525
 Arg Ala Arg Asp Val Thr Lys Arg Val Val Gly Ser Thr Val Pro Val
 530 535 540
 Leu Asp Gly Glu Ala Leu Ser Met Arg Val Leu Val Asp His Ser Ile
 545 550 555 560
 Val Gln Ser Phe Ala Met Gly Gly Arg Val Thr Ala Thr Ser Arg Val
 565 570 575
 Tyr Pro Thr Glu Ala Ile Tyr Ala Arg Ala Gly Val Tyr Leu Phe Asn
 580 585 590
 Asn Ala Thr Gly Ala Ser Val Thr Ala Glu Arg Leu Ile Val His Glu
 595 600 605
 Met Ala Ser Ala Val Tyr Asp Glu Thr Leu Met Val Gln Asp Ser
 610 615 620

<210> 68

<211> 619

<212> PRT

<213> Lolium perenne

<400> 68

Met Glu Ser Arg Asp Phe Pro Ser Ala Ala Tyr Ala Pro Leu Leu Pro
 1 5 10 15
 Ser Ala Ala Asp Asp Val Ala Leu Ala Lys Gln Asp Arg Pro Gly Val
 20 25 30
 Gly Trp Arg Gly Phe Leu Thr Val Leu Ala Ala Cys Gly Val Val Val
 35 40 45
 Leu Leu Val Ala Ala Ser Leu Leu Ala Gly Ser Arg Met Gly Gln Ala
 50 55 60
 Gly Asp Thr Asp Glu Asp Gly Ala Gly Gly Phe Pro Trp Ser Asn Glu
 65 70 75 80
 Met Leu Gln Trp Gln Arg Ala Gly Phe His Tyr Gln Pro Glu Gly His
 85 90 95
 Phe Met Ser Asp Pro Asp Gly Pro Val Tyr Tyr Arg Gly Tyr Tyr His
 100 105 110
 Leu Phe Phe Gln Tyr Asn Arg Arg Gly Val Ala Trp Asp Asp Tyr Ile
 115 120 125

Glu Trp Gly His Val Val Ser Gln Asp Leu Val His Trp Arg Pro Leu
 130 135 140
 Pro Leu Ala Met Arg Pro Asp His Trp Tyr Asp Lys Lys Gly Val Leu
 145 150 155 160
 Ser Gly Thr Ile Thr Val Leu His Asn Gly Thr Leu Val Leu Leu Tyr
 165 170 175
 Thr Gly Val Thr Glu Asp Pro Met Ala Glu Ser Gln Cys Ile Ala Val
 180 185 190
 Pro Thr Asp Pro Asn Asp Pro Leu Leu Arg His Trp Thr Lys His Pro
 195 200 205
 Ala Asn Pro Val Leu Ala His Pro Gln Gly Val Gln Gly Met Asp Phe
 210 215 220
 Arg Asp Pro Thr Ser Ala Trp Trp Asp Lys Ser Asp Ser Thr Trp Arg
 225 230 235 240
 Ile Leu Ile Gly Ser Lys Asp Asp Asp Asn Gly Ser His Ala Gly Ile
 245 250 255
 Ala Phe Ile Phe Lys Thr Lys Asp Phe Leu Ile Phe Glu Arg Val Pro
 260 265 270
 Gly Ile Val His Arg Val Glu Gly Thr Gly Met Trp Glu Cys Ile Asp
 275 280 285
 Phe Tyr Pro Val Gly Gly Gly His Asn Ser Ser Ser Glu Glu Leu Tyr
 290 295 300
 Val Ile Lys Ala Ser Met Asp Asp Glu Arg His Asp Tyr Tyr Ser Leu
 305 310 315 320
 Gly Arg Tyr Asp Ala Ala Ala Asn Thr Trp Thr Pro Leu Asp Ala Glu
 325 330 335
 Leu Asp Leu Gly Ile Gly Leu Arg Tyr Asp Trp Gly Lys Leu Tyr Ala
 340 345 350
 Ser Thr Ser Phe Tyr Asp Pro Leu Lys Gln Arg Arg Ile Met Leu Gly
 355 360 365
 Tyr Val Gly Asp Val Asp Ser Ala Arg Ala Asp Val Ala Lys Gly Trp
 370 375 380
 Ala Ser Leu Gln Ser Ile Pro Arg Thr Val Ala Leu Asp Glu Lys Thr
 385 390 395 400
 Arg Thr Asn Leu Leu Leu Trp Pro Val Glu Glu Val Glu Ala Leu Arg
 405 410 415
 Tyr Asn Ser Thr Asp Leu Ser Gly Ile Thr Val Glu Asn Gly Ser Ile
 420 425 430
 Phe His Leu Pro Leu His Gln Ala Thr Gln Leu Asp Ile Glu Ala Ser
 435 440 445
 Phe Arg Leu Asp Ala Ser Asp Val Ala Ala Ile Asn Glu Ala Asp Val
 450 455 460
 Gly Tyr Asn Cys Ser Ser Ser Gly Gly Ala Ala Ala Arg Gly Ala Leu
 465 470 475 480
 Gly Pro Phe Gly Leu Leu Val His Ala Ala Gly Asp Leu Arg Gly Glu
 485 490 495
 Gln Thr Ala Val Tyr Phe Tyr Val Ser Arg Ala Leu Asp Gly Ser Leu
 500 505 510
 Arg Thr Ser Phe Cys Asn Asp Glu Thr Arg Ser Ser Arg Ala Arg Asp
 515 520 525
 Val Ala Lys Arg Val Val Gly Ser Thr Val Pro Val Leu Asp Gly Glu
 530 535 540
 Val Leu Ala Met Arg Val Leu Val Asp His Ser Ile Val Gln Ser Phe
 545 550 555 560
 Ala Met Gly Gly Arg Val Thr Ala Thr Ser Arg Val Tyr Pro Thr Glu
 565 570 575
 Ala Ile Tyr Ala Arg Ala Gly Val Tyr Leu Phe Asn Asn Ala Thr Gly
 580 585 590
 Ala Ser Val Thr Ala Glu Arg Leu Ile Val His Glu Met Ala Ser Ala
 595 600 605
 Val Tyr Asp Glu Thr Val Met Val Lys Asp Ser
 610 615

<210> 69

<211> 422

<212> PRT

<213> Festuca arundinacea

<400> 69

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Met Asp Lys Leu Asn Gly Ser Ala Arg Leu Met Ile Val Ser Asp Leu
 1          5          10          15
Asp His Thr Met Val Asp His His Asp Glu Glu Asn Leu Ser Leu Leu
          20          25          30
Arg Phe Gly Ala Leu Trp Glu Ser Ala Tyr Cys Gln Asp Ser Leu Leu
          35          40          45
Val Phe Ser Thr Gly Arg Ser Pro Thr Leu Tyr Lys Glu Leu Arg Lys
 50          55          60
Glu Lys Pro Met Leu Thr Pro Asp Ile Thr Ile Met Ser Val Gly Ser
 65          70          75          80
Glu Ile Thr Tyr Gly Glu Ala Met Val Pro Asp Asp Gly Trp Glu Glu
          85          90          95
Tyr Leu Asn Asn Lys Trp Asp Arg Asn Ile Val Leu Glu Glu Thr Ala
          100          105          110
Lys Tyr Ser Glu Leu Lys Leu Gln Pro Glu Thr Glu Gln Arg Pro His
          115          120          125
Lys Val Ser Phe Leu Val Asp Lys Lys Ser Ala Gln Glu Val Ile Lys
 130          135          140
Ser Leu Ser Glu Lys Phe Glu Lys Arg Gly Val Asp Ala Lys Ile Ile
 145          150          155          160
Tyr Ser Gly Gly Gln Asp Leu Asp Ile Leu Ala Gln Gly Ala Gly Lys
          165          170          175
Gly Gln Ala Leu Ala Tyr Leu Leu Lys Lys Phe Ala Ser Cys Gly Lys
          180          185          190
Thr Pro Asn Asn Thr Leu Val Cys Gly Asp Ser Gly Asn Asp Ala Glu
          195          200          205
Leu Phe Ser Ile Pro Gly Val His Gly Val Met Val Ser Asn Ala Gln
 210          215          220
Glu Glu Leu Leu Gln Trp His Ala Glu Asn Ala Lys Asp Asn Pro Lys
 225          230          235          240
Val Ile His Ala Thr Glu Arg Cys Ala Ala Gly Ile Ile Gln Ala Ile
          245          250          255
Gly His Phe Lys Leu Gly Pro Asn Ile Ser Pro Arg Asp Ile Glu Phe
          260          265          270
Pro Tyr Val Lys Glu Asp Ser Phe Lys Pro Thr Ala Ala Val Val Lys
          275          280          285
Phe Tyr Val Leu Cys Glu Lys Trp Arg Arg Ala Asp Val Pro Lys Ala
          290          295          300
Asp Ser Val Ile Glu Tyr Phe Lys Asn Ile Thr Asp Ala Ser Gly Val
 305          310          315          320
Ile Ile His Pro Ser Gly Leu Glu Leu Ser Ile His Ser Ser Ile Asp
          325          330          335
Ala Leu Ala Ser Cys Tyr Gly Asp Lys Gln Gly Lys Lys Tyr Arg Ser
          340          345          350
Trp Val Asp Arg Leu Val Ile Ser Gln Thr Ala Ser Asp Ser Trp Leu
          355          360          365
Val Arg Phe Asp Leu Trp Glu Ala Glu Gly Asp Ala Trp Val Cys Cys
 370          375          380
Leu Thr Thr Leu Ala Leu Asn Val Lys Pro Glu Thr Pro Gly Gly Phe
 385          390          395          400
Val Val Thr His Ile His Lys Thr Trp Leu Lys Glu Tyr Ser Gly Asp
          405          410          415
Glu Gln Ala Ser Lys Leu
          420

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<210> 70

<211> 422

<212> PRT

<213> Lolium perenne

<400> 70

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Met Asp Lys Leu Asn Gly Ser Ala Arg Leu Met Ile Val Ser Asp Leu
 1          5          10          15
Asp His Thr Met Val Asp His His Asp Glu Glu Asn Leu Ser Leu Leu
          20          25          30
Arg Phe Gly Ala Leu Trp Glu Ser Thr Tyr Cys Gln Asp Ser Leu Leu
          35          40          45
Val Phe Ser Thr Gly Arg Ser Pro Thr Leu Tyr Lys Glu Leu Arg Lys
          50          55          60
Glu Lys Pro Met Leu Thr Pro Asp Ile Thr Ile Met Ser Val Gly Ser
          65          70          75          80
Glu Ile Thr Tyr Gly Glu Ala Met Val Pro Asp Asp Gly Trp Glu Glu
          85          90          95
Tyr Leu Asn Asn Lys Trp Asp Lys Ser Ile Val Leu Glu Glu Thr Ala
          100          105          110
Lys Phe Ser Glu Leu Lys Leu Gln Ala Glu Thr Glu Gln Arg Pro His
          115          120          125
Lys Val Ser Phe Leu Val Asp Lys Lys Thr Ala Gln Glu Val Ile Lys
          130          135          140
Ser Leu Ser Glu Lys Phe Glu Lys Arg Gly Val Asp Ala Lys Ile Ile
          145          150          155          160
Tyr Ser Gly Gly Gln Asp Leu Asp Ile Leu Ala Gln Gly Ala Gly Lys
          165          170          175
Gly Gln Ala Leu Ala Tyr Leu Leu Lys Lys Phe Ala Ser Cys Gly Lys
          180          185          190
Thr Pro Asn Asn Thr Leu Val Cys Gly Asp Ser Gly Asn Asp Ala Glu
          195          200          205
Leu Phe Ser Ile Pro Gly Val His Gly Val Met Val Ser Asn Ala Gln
          210          215          220
Glu Glu Leu Leu Gln Trp Arg Ala Glu Asn Ala Lys Asp Asn Pro Lys
          225          230          235          240
Val Ile His Ala Thr Glu Arg Cys Ala Ala Gly Ile Ile Gln Ala Ile
          245          250          255
Gly His Phe Lys Leu Gly Pro Asn Val Ser Pro Arg Asp Val Glu Phe
          260          265          270
Pro Tyr Val Lys Glu Asp Ser Phe Lys Pro Thr Ala Ala Val Val Lys
          275          280          285
Phe Tyr Val Leu Cys Glu Lys Trp Arg Arg Ala Asp Val Pro Lys Thr
          290          295          300
Asp Ser Val Ile Glu Tyr Phe Lys Asn Ile Thr Asp Ala Ser Gly Val
          305          310          315          320
Ile Ile His Pro Ser Gly Leu Glu Leu Ser Ile His Ser Ser Ile Asp
          325          330          335
Ala Leu Ala Ser Cys Tyr Gly Asp Lys Gln Gly Lys Lys Tyr Arg Ser
          340          345          350
Trp Val Asp Arg Leu Val Ile Ser Gln Thr Ala Ser Asp Ser Trp Leu
          355          360          365
Val Arg Phe Asp Leu Trp Glu Ala Glu Gly Asp Lys Trp Val Cys Cys
          370          375          380
Leu Thr Thr Leu Ala Leu Asn Val Lys Pro Glu Thr Pro Gly Gly Phe
          385          390          395          400
Val Val Thr His Ile His Lys Thr Trp Leu Lys Glu Tyr Ser Gly Asp
          405          410          415
Glu Gln Ala Ser Lys Leu
          420

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<210> 71

<211> 1062

<212> PRT

<213> Festuca arundinacea

<400> 71

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Met Ala Ala Gly Asn Glu Trp Ile Asn Gly Tyr Leu Glu Ala Ile Leu
 1          5          10          15
Asp Ala Gly Ser Lys Leu Arg Pro Gln Gly Val Gln Leu Pro Pro Leu
          20          25          30

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Glu	Thr	Ala	Pro	Ala	Leu	Ala	Ala	Glu	Glu	Ser	Gly	Ala	Ala	Tyr	Asn
		35					40					45			
Pro	Thr	Arg	Tyr	Phe	Val	Glu	Glu	Val	Val	Arg	Ser	Phe	Asp	Glu	Gln
	50					55					60				
Ala	Leu	His	Lys	Thr	Trp	Thr	Lys	Val	Val	Ala	Met	Arg	Asn	Ser	Gln
	65				70					75					80
Glu	Arg	Ser	Asn	Arg	Leu	Glu	Asn	Leu	Cys	Trp	Arg	Ile	Trp	Asn	Val
			85						90					95	
Ser	Arg	Gln	Lys	Lys	Gln	Val	Glu	Trp	Asp	Tyr	Thr	Lys	Glu	Val	Ala
			100					105					110		
Arg	Arg	Lys	Leu	Glu	Gln	Glu	Leu	Gly	Ser	Arg	Glu	Ala	Ala	Glu	Asp
		115					120					125			
Leu	Ser	Glu	Leu	Ser	Glu	Gly	Glu	Lys	Asp	Thr	Thr	Ala	Lys	Pro	
	130					135						140			
Asp	Ala	Ala	Thr	Ala	Gln	Pro	Ser	Thr	Asp	Asp	Gly	Glu	His	Gln	Gln
	145				150					155					160
Pro	Gln	Pro	Arg	Thr	Arg	Leu	Ala	Arg	Ile	Asn	Ser	Glu	Val	Arg	Leu
			165						170					175	
Val	Ser	Asp	Asp	Glu	Glu	Glu	Gln	Thr	Lys	Lys	Arg	Asn	Leu	Tyr	Ile
			180					185					190		
Val	Leu	Ile	Ser	Ile	His	Gly	Leu	Val	Arg	Gly	Glu	Asn	Met	Glu	Leu
	195						200					205			
Gly	Arg	Asp	Ser	Asp	Thr	Gly	Gly	Gln	Val	Lys	Tyr	Val	Val	Glu	Leu
	210					215					220				
Ala	Arg	Ala	Leu	Ala	Ala	Thr	Ala	Gly	Val	His	Arg	Val	Asp	Leu	Leu
	225				230					235					240
Thr	Arg	Gln	Ile	Ser	Cys	Pro	Asp	Val	Asp	Trp	Thr	Tyr	Gly	Glu	Pro
			245						250					255	
Val	Glu	Met	Leu	Glu	Arg	Leu	Ser	Ser	Ala	Asp	Ala	Asp	Glu	Asp	Asp
			260					265					270		
Gly	Glu	Gln	Ser	Gly	Gly	Gly	Ala	Tyr	Ile	Val	Arg	Leu	Pro	Cys	Gly
	275						280					285			
Pro	Arg	Asp	Gln	Tyr	Ile	Pro	Lys	Glu	Glu	Leu	Trp	Pro	His	Ile	Pro
	290					295					300				
Glu	Phe	Val	Asp	Arg	Ala	Leu	Ser	His	Val	Thr	Glu	Val	Ala	Arg	Ala
	305				310					315					320
Leu	Gly	Asp	Gln	Leu	Gln	Pro	Pro	Pro	Thr	Pro	Ala	Ala	Gly	Asp	Gly
			325						330					335	
Ala	Ala	Leu	Val	Ala	Ala	Pro	Ile	Trp	Pro	Tyr	Val	Ile	His	Gly	His
			340					345					350		
Tyr	Ala	Asp	Ala	Ala	Glu	Val	Ala	Ala	Asn	Leu	Ala	Ser	Ala	Leu	Asn
	355						360					365			
Val	Pro	Met	Val	Met	Thr	Gly	His	Ser	Leu	Gly	Arg	Asn	Lys	Leu	Glu
	370					375					380				
Gln	Leu	Leu	Lys	Leu	Gly	Arg	Met	Pro	Gly	Pro	Glu	Ile	Gln	Gly	Thr
	385				390					395					400
Tyr	Lys	Ile	Ala	Arg	Arg	Ile	Glu	Ala	Glu	Glu	Thr	Gly	Leu	Asp	Thr
			405						410					415	
Ala	Glu	Met	Val	Val	Thr	Ser	Thr	Lys	Gln	Glu	Ile	Glu	Glu	Gln	Trp
			420					425					430		
Gly	Leu	Tyr	Asp	Gly	Phe	Asp	Leu	Met	Val	Glu	Arg	Lys	Leu	Arg	Val
	435						440					445			
Arg	Gln	Arg	Arg	Gly	Val	Ser	Ser	Leu	Gly	Arg	Tyr	Met	Pro	Arg	Met
	450					455					460				
Ala	Val	Ile	Pro	Pro	Gly	Met	Asp	Phe	Ser	Phe	Val	Glu	Thr	Gln	Asp
	465				470					475					480
Thr	Ala	Glu	Gly	Asp	Gly	Ala	Asp	Leu	Gln	Met	Leu	Ile	Ala	Pro	Asp
			485						490					495	
Lys	Ala	Lys	Lys	Ala	Leu	Pro	Pro	Ile	Trp	Ser	Asp	Val	Leu	Arg	Phe
			500					505					510		
Phe	Thr	Asn	Pro	His	Lys	Pro	Met	Ile	Leu	Ala	Leu	Ser	Arg	Pro	Asp
	515						520					525			
Pro	Lys	Lys	Asn	Val	Thr	Thr	Leu	Leu	Lys	Ala	Tyr	Gly	Glu	Ser	Arg
	530					535					540				
Gln	Leu	Arg	Glu	Leu	Ala	Asn	Leu	Thr	Leu	Ile	Leu	Gly	Asn	Arg	Asp
	545				550					555					560

Asp Ile Glu Asp Met Ala Gly Gly Gly Gly Ala Val Leu Thr Ala Val
 565 570 575
 Leu Lys Leu Ile Asp Arg Tyr Asp Leu Tyr Gly Gln Val Ala Tyr Pro
 580 585 590
 Lys His His Lys Gln Thr Asp Val Pro His Ile Tyr Arg Leu Ala Ala
 595 600 605
 Lys Thr Lys Gly Val Phe Thr Asn Pro Ala Leu Val Glu Pro Phe Gly
 610 615 620
 Leu Thr Ile Ile Glu Ala Ala Ala Tyr Gly Leu Pro Val Val Ala Thr
 625 630 635 640
 Lys Asn Gly Gly Pro Val Asp Ile Leu Lys Ala Leu Asn Asn Gly Leu
 645 650 655
 Leu Val Asp Pro His Ser Ala Glu Ala Ile Thr Gly Ala Leu Leu Ser
 660 665 670
 Leu Leu Ala Glu Lys Ser Arg Trp Val Glu Cys Arg Arg Asn Gly Leu
 675 680 685
 Arg Asn Ile His Arg Phe Ser Trp Pro His His Cys Arg Leu Tyr Leu
 690 695 700
 Ser His Val Ser Thr Tyr Cys Asp Gln Pro Ser Pro His Gln Pro Leu
 705 710 715 720
 Arg Val Pro Leu Gly Leu Gly Ser Ser Thr Ser Phe Gly Ala Asp Asp
 725 730 735
 Ser Leu Ser Asp Ser Leu Arg Gly Leu Ser Leu Gln Ile Ser Val Asp
 740 745 750
 Ala Ser Ser Asp Leu Asn Ala Ala Asp Ser Ala Ala Ile Met Asp
 755 760 765
 Ala Leu Arg Arg Arg Pro Ala Ser Glu Lys Pro Ala Ser Ser Gly Ala
 770 775 780
 Arg Ala Leu Gly Phe Ala Pro Gly Arg Arg Glu Ser Leu Leu Val Val
 785 790 795 800
 Ala Val Asp Cys Tyr Gly Asp Asp Gly Lys Pro Asp Val Lys Gln Leu
 805 810 815
 Lys Lys Ala Ile Asp Ala Ala Val Ser Val Gly Glu Cys Ala Gly Ala
 820 825 830
 Lys Gln Gly Tyr Val Leu Ser Thr Gly Met Thr Ile Pro Glu Ala Ala
 835 840 845
 Glu Ala Ile Lys Ala Cys Gly Ala Asp Val Ala Ser Phe Asp Ala Leu
 850 855 860
 Ile Cys Ser Ser Gly Ala Glu Leu Cys Tyr Pro Trp Lys Glu Leu Ala
 865 870 875 880
 Ala Asp Glu Glu Tyr Ser Gly His Val Ala Phe Arg Trp Pro Gly Asp
 885 890 895
 His Val Lys Ser Ala Val Pro Arg Leu Gly Ser Leu Glu Glu Ile Ala
 900 905 910
 Leu Ala Ile Asp Arg Pro Ala Cys Ser Val His Cys His Ala Tyr Ala
 915 920 925
 Ala Thr Asp Ala Ser Lys Val Lys Lys Val Asp Ser Ile Arg Lys Ser
 930 935 940
 Leu Arg Met Arg Gly Phe Arg Cys Asn Leu Val Tyr Thr Arg Ala Cys
 945 950 955 960
 Thr Arg Leu Asn Val Ile Pro Leu Ser Ala Ser Arg Pro Arg Ala Leu
 965 970 975
 Arg Tyr Leu Ser Ile Gln Trp Gly Ile Asp Leu Ser Lys Val Ala Val
 980 985 990
 Leu Val Gly Glu Thr Gly Asp Thr Asp Arg Glu Arg Leu Leu Pro Gly
 995 1000 1005
 Val His Lys Thr Leu Ile Leu Pro Gly Met Val Ala Arg Gly Ser Glu
 1010 1015 1020
 Glu Leu Leu Arg Gly Asp Asp Gly Tyr Thr Met Ala Asp Val Val Ala
 1025 1030 1035 1040
 Met Asp Ser Pro Asn Ile Val Thr Leu Ala Glu Gly Gln Ser Ala Ser
 1045 1050 1055
 Asp Leu Leu Lys Ala Ile
 1060

<210> 72
 <211> 1074
 <212> PRT
 <213> Lolium perenne

<400> 72
 Met Ala Gly Asn Asp Trp Ile Asn Ser Tyr Leu Glu Ala Ile Leu Asp
 1 5 10 15
 Ala Gly Gly Thr Ala Gly Asp Ile Ser Ala Ala Ser Val Ala Gly Gly
 20 25 30
 Asp Asp Gly Pro Gly Ala Gly Gly Thr Ala Gly Glu Lys Arg Asp
 35 40 45
 Lys Ser Ser Leu Met Leu Arg Glu Arg Gly Arg Phe Asn Pro Ala Arg
 50 55 60
 Tyr Phe Val Glu Glu Val Ile Ser Gly Phe Asp Glu Thr Asp Leu Tyr
 65 70 75 80
 Lys Thr Trp Val Arg Thr Ser Ala Met Arg Ser Pro Gln Glu Arg Asn
 85 90 95
 Thr Arg Leu Glu Asn Met Ser Trp Arg Ile Trp Asn Leu Ala Arg Lys
 100 105 110
 Lys Lys Gln Ile Glu Gly Glu Glu Ala Ser Arg Leu Ser Lys Lys Arg
 115 120 125
 Leu Glu Arg Glu Lys Ala Arg Arg Asp Ala Ala Ala Asp Leu Ser Glu
 130 135 140
 Asp Leu Ser Glu Gly Glu Lys Gly Glu Asn Ile Asn Gly Ser Ser Val
 145 150 155 160
 His Asp Glu Ser Thr Arg Gly Arg Met Pro Arg Ile Gly Ser Thr Asp
 165 170 175
 Ala Ile Glu Val Trp Ala Asn Gln His Lys Asp Lys Lys Leu Tyr Ile
 180 185 190
 Val Leu Ile Ser Ile His Gly Leu Ile Arg Gly Glu Asn Met Glu Leu
 195 200 205
 Gly Arg Asp Ser Asp Thr Gly Gly Gln Val Lys Tyr Val Val Glu Leu
 210 215 220
 Ala Arg Ala Leu Gly Glu Thr Pro Gly Val Tyr Arg Val Asp Leu Leu
 225 230 235 240
 Thr Arg Gln Ile Ser Ala Pro Asp Val Asp Trp Ser Tyr Gly Glu Pro
 245 250 255
 Thr Glu Met Leu Ser Pro Arg Asn Ser Glu Asn Leu Gly Asp Asp Met
 260 265 270
 Gly Glu Ser Ser Gly Ala Tyr Ile Val Arg Ile Pro Phe Gly Pro Arg
 275 280 285
 Glu Lys Tyr Ile Pro Lys Glu Gln Leu Trp Pro His Ile Gln Glu Phe
 290 295 300
 Val Asp Gly Ala Leu Val His Ile Met Gln Met Ser Lys Val Leu Gly
 305 310 315 320
 Glu Gln Val Gly Arg Glu Arg Arg Val Trp Pro Val Val Ile His Gly
 325 330 335
 His Tyr Ala Asp Ala Gly Asp Ser Ala Ala Leu Leu Ser Gly Ala Leu
 340 345 350
 Asn Val Pro Met Val Phe Thr Gly His Ser Leu Gly Arg Asp Lys Leu
 355 360 365
 Glu Gln Leu Leu Lys Gln Gly Arg Gln Thr Arg Asp Glu Val Asn Ala
 370 375 380
 Thr Tyr Lys Ile Met Arg Arg Ile Glu Ala Glu Leu Cys Leu Asp
 385 390 395 400
 Ala Ser Glu Ile Val Ile Thr Ser Thr Arg Gln Glu Ile Glu Lys Gln
 405 410 415
 Trp Gly Leu Tyr Asn Gly Phe Asp Val Thr Met Glu Arg Lys Leu Arg
 420 425 430
 Ala Arg Thr Lys Arg Gly Val Ser Cys Tyr Gly Arg Tyr Met Pro Arg
 435 440 445
 Met Ile Ala Ile Pro Pro Gly Met Glu Phe Ser His Ile Val Pro His
 450 455 460
 Asp Val Asp Leu Asp Gly Asp Glu Ala Asn Glu Val Gly Ser Gly Ser
 465 470 475 480

Pro	Asp	Pro	Pro	Ile	Trp	Ala	Asp	Ile	Met	Arg	Phe	Phe	Ser	Asn	Pro		
				485					490					495			
Arg	Lys	Pro	Met	Ile	Leu	Ala	Leu	Ala	Arg	Pro	Asp	Pro	Lys	Lys	Asn		
			500					505					510				
Ile	Thr	Thr	Leu	Val	Lys	Ala	Phe	Gly	Glu	His	Pro	Gly	Leu	Arg	Asn		
		515					520					525					
Leu	Ala	Asn	Leu	Thr	Leu	Ile	Met	Gly	Asn	Arg	Asp	Val	Ile	Asp	Glu		
	530					535					540						
Met	Ser	Ser	Thr	Asn	Gly	Ala	Val	Leu	Thr	Ser	Val	Leu	Lys	Leu	Ile		
545					550					555					560		
Asp	Lys	Tyr	Asp	Leu	Tyr	Gly	Gln	Val	Ala	Tyr	Pro	Lys	His	His	Lys		
				565					570					575			
Gln	Ser	Glu	Val	Pro	Asp	Ile	Tyr	Arg	Leu	Ala	Ala	Arg	Thr	Lys	Gly		
			580					585					590				
Val	Phe	Ile	Asn	Cys	Ala	Tyr	Ile	Glu	Pro	Phe	Gly	Leu	Thr	Leu	Ile		
		595					600					605					
Glu	Ala	Ala	Ala	Tyr	Gly	Leu	Pro	Met	Val	Ala	Thr	Gln	Asn	Gly	Gly		
	610					615						620					
Pro	Val	Asp	Ile	His	Arg	Val	Leu	Asp	Asn	Gly	Ile	Leu	Val	Asp	Pro		
625					630					635					640		
His	Asn	Gln	Asn	Asp	Ile	Ala	Glu	Ala	Leu	Tyr	Lys	Leu	Val	Ser	Asp		
				645					650					655			
Lys	His	Leu	Trp	Ala	Gln	Cys	Arg	Gln	Asn	Gly	Leu	Asp	Asn	Ile	His		
			660					665					670				
Arg	Phe	Ser	Trp	Pro	Glu	His	Cys	Lys	Asn	Tyr	Leu	Ser	Arg	Val	Gly		
		675					680						685				
Thr	Val	Lys	Pro	Arg	His	Pro	Arg	Trp	Gln	Arg	Ser	Asp	Asp	Ala	Thr		
		690				695						700					
Glu	Val	Ser	Glu	Ser	Asp	Ser	Pro	Gly	Asp	Ser	Leu	Arg	Asp	Val	His		
705					710					715					720		
Asp	Ile	Ser	Leu	Asn	Leu	Lys	Leu	Ser	Leu	Asp	Ser	Glu	Lys	Ala	Gly		
				725					730					735			
Thr	Lys	Ile	Asn	Thr	Glu	Arg	Asn	Ser	Thr	Asn	Ala	Arg	Arg	Asn	Leu		
			740					745					750				
Glu	Asp	Ala	Val	Leu	Lys	Phe	Ser	Asn	Ala	Val	Ser	Glu	Gly	Thr	Lys		
		755					760					765					
Asp	Glu	Ser	Asp	Glu	Asn	Ala	Glu	Ala	Thr	Thr	Gly	Ser	Ile	Asn	Gly		
	770					775						780					
His	Leu	Tyr	Gly	Glu	Lys	His	Ile	Val	Val	Ile	Ala	Val	Asp	Ser	Val		
785					790					795					800		
Gln	Asn	Ala	Asp	Leu	Val	Gln	Ile	Ile	Lys	Asn	Leu	Phe	Glu	Ala	Ser		
				805					810					815			
Arg	Lys	Glu	Lys	Ser	Ser	Gly	Ala	Val	Gly	Phe	Val	Leu	Ser	Thr	Ser		
			820					825						830			
Arg	Ala	Ile	Ser	Glu	Thr	Leu	Thr	Phe	Leu	Thr	Ser	Gly	Gly	Ile	Gln		
		835					840						845				
Thr	Thr	Glu	Phe	Asp	Ala	Phe	Ile	Cys	Ser	Ser	Gly	Ser	Asp	Leu	Cys		
		850				855						860					
Tyr	Pro	Ser	Ser	Ser	Ser	Glu	Asp	Met	Leu	Ser	Pro	Thr	Glu	Leu	Pro		
865					870					875					880		
Phe	Met	Ile	Asp	Leu	Asp	Tyr	His	Ser	Gln	Ile	Glu	Tyr	Arg	Trp	Gly		
				885					890					895			
Gly	Glu	Gly	Leu	Arg	Lys	Thr	Leu	Ile	Arg	Trp	Ala	Ala	Glu	Asn	Asn		
			900					905					910				
Ser	Gln	Ser	Gly	Gln	Glu	Val	Val	Thr	Glu	Asp	Glu	Glu	Cys	Ser	Ser		
		915						920					925				
Thr	Tyr	Cys	Ile	Ser	Phe	Lys	Val	Lys	Asn	Thr	Glu	Ala	Val	Pro	Pro		
		930				935						940					
Val	Lys	Asp	Leu	Arg	Lys	Thr	Met	Arg	Ile	Gln	Ala	Leu	Arg	Cys	His		
945					950					955					960		
Val	Leu	Tyr	Ser	His	Asp	Gly	Ser	Lys	Leu	Asn	Leu	Ile	Pro	Leu	Leu		
				965					970					975			
Ala	Ser	Arg	Ser	Gln	Ala	Leu	Arg	Tyr	Leu	Tyr	Ile	Arg	Trp	Gly	Val		
			980					985					990				
Glu	Leu	Ala	Asn	Met	Thr	Val	Val	Val	Gly	Glu	Ser	Gly	Asp	Thr	Asp		
			995					1000					1005				

Tyr Glu Gly Leu Leu Gly Gly Val His Lys Thr Ile Ile Leu Lys Gly
 1010 1015 1020
 Ser Phe Asn Ala Ala Pro Asn Gln Leu His Ala Ala Arg Ser Tyr Ser
 1025 1030 1035 1040
 Leu Glu Asp Val Ile Ser Phe Asp Lys Pro Gly Ile Ala Ser Val Glu
 1045 1050 1055
 Gly Tyr Leu Pro Asp Ser Leu Lys Ser Ala Leu Gln Gln Phe Gly Val
 1060 1065 1070
 Leu Asn

<210> 73
 <211> 937
 <212> PRT
 <213> *Lolium perenne*

<400> 73
 Met Ala Ala Gly Asn Glu Trp Ile Asn Gly Tyr Leu Glu Ala Ile Leu
 1 5 10 15
 Asp Ala Gly Ser Lys Leu Arg Pro Gln Gly Val Gln Leu Pro Pro Leu
 20 25 30
 Glu Thr Ala Pro Ala Leu Ala Ala Glu Glu Ser Ser Ala Ala Tyr Asn
 35 40 45
 Pro Thr Arg Tyr Phe Val Glu Glu Val Val Arg Ser Phe Asp Glu Gln
 50 55 60
 Ala Leu His Lys Thr Trp Thr Lys Val Val Ala Met Arg Asn Ser Gln
 65 70 75 80
 Glu Arg Ser Asn Arg Leu Glu Asn Leu Cys Trp Arg Ile Trp Asn Val
 85 90 95
 Ser Arg Gln Lys Lys Gln Val Glu Trp Asp Tyr Thr Lys Glu Val Ala
 100 105 110
 Arg Arg Lys Leu Glu Gln Glu Leu Gly Ser Arg Glu Ala Ala Glu Asp
 115 120 125
 Leu Ser Glu Leu Ser Glu Gly Glu Lys Asp Thr Thr Thr Ala Lys Pro
 130 135 140
 Asp Ala Ala Ala Ala Gln Pro Ser Ala Asp Asp Gly Glu His Gln Gln
 145 150 155 160
 Pro Gln Pro Arg Thr Arg Leu Ala Arg Ile Asn Ser Glu Val Arg Leu
 165 170 175
 Val Ser Asp Asp Glu Glu Glu Gln Thr Lys Lys Arg Asn Leu Tyr Ile
 180 185 190
 Val Leu Ile Ser Ile His Gly Leu Val Arg Gly Glu Asn Met Glu Leu
 195 200 205
 Gly Arg Asp Ser Asp Thr Gly Gly Gln Val Lys Tyr Val Val Glu Leu
 210 215 220
 Ala Arg Ala Leu Ala Ala Thr Ala Gly Val His Arg Val Asp Leu Leu
 225 230 235 240
 Thr Arg Gln Ile Ser Cys Pro Asp Val Asp Trp Thr Tyr Gly Glu Pro
 245 250 255
 Val Glu Met Leu Glu Arg Leu Ser Ser Ala Asp Ala Asp Asp Asp
 260 265 270
 Gly Glu Gln Ala Gly Gly Gly Ala Tyr Ile Val Arg Leu Pro Cys Gly
 275 280 285
 Pro Arg Asp Gln Tyr Ile Pro Lys Glu Glu Leu Trp Pro His Ile Pro
 290 295 300
 Glu Phe Val Asp Arg Ala Leu Ser His Val Thr Glu Val Ala Arg Ala
 305 310 315 320
 Leu Gly Glu Gln Leu Gln Pro Pro Pro Ser Pro Ala Asp Gly Ala Val
 325 330 335
 Ala Ala Pro Ile Trp Pro Tyr Val Ile His Gly His Tyr Ala Asp Ala
 340 345 350
 Ala Glu Val Ala Ala Asn Leu Ala Ser Ala Leu Asn Val Pro Met Val
 355 360 365
 Met Thr Gly His Ser Leu Gly Arg Asn Lys Leu Glu Gln Leu Leu Lys
 370 375 380

Leu Gly Arg Met Pro Gly Pro Glu Ile Gln Gly Thr Tyr Lys Ile Ala
 385 390 395 400
 Arg Arg Ile Glu Ala Glu Glu Thr Gly Leu Asp Thr Ala Glu Met Val
 405 410 415
 Val Thr Ser Thr Lys Gln Glu Ile Glu Glu Gln Trp Gly Leu Tyr Asp
 420 425 430
 Gly Phe Asp Leu Met Val Glu Arg Lys Leu Arg Val Arg Gln Arg Arg
 435 440 445
 Gly Val Ser Ser Leu Gly Arg Tyr Met Pro Arg Met Ala Val Ile Pro
 450 455 460
 Pro Gly Met Asp Phe Ser Phe Val Glu Thr Gln Asp Thr Ala Asp Gly
 465 470 475 480
 Thr Gly Arg Ser Gln Met Leu Ile Ala Pro Asp Lys Ala Lys Lys Ala
 485 490 495
 Leu Pro Pro Ile Trp Ser Asp Val Leu Arg Phe Phe Thr Asn Pro His
 500 505 510
 Lys Pro Met Ile Leu Ala Leu Ser Arg Pro Asp Pro Lys Lys Asn Val
 515 520 525
 Thr Thr Leu Leu Lys Ala Tyr Gly Glu Ser Arg Gln Leu Arg Glu Leu
 530 535 540
 Ala Asn Leu Thr Leu Ile Leu Gly Asn Arg Asp Asp Ile Glu Asp Met
 545 550 555 560
 Ala Gly Gly Gly Gly Ala Val Leu Thr Ala Val Leu Lys Leu Ile Asp
 565 570 575
 Arg Tyr Asp Leu Tyr Gly Gln Val Ala Tyr Pro Lys His His Lys Gln
 580 585 590
 Thr Asp Val Pro His Ile Tyr Arg Leu Ala Ala Lys Thr Lys Gly Val
 595 600 605
 Phe Ile Asn Pro Ala Leu Val Glu Pro Phe Gly Leu Thr Ile Ile Glu
 610 615 620
 Ala Ala Ala Tyr Gly Leu Pro Val Val Ala Thr Lys Asn Gly Gly Pro
 625 630 635 640
 Val Asp Ile Leu Lys Ala Leu His Asn Gly Leu Leu Val Asp Pro His
 645 650 655
 Ser Ala Glu Ala Ile Thr Gly Ala Leu Leu Ser Leu Leu Ala Glu Lys
 660 665 670
 Ser Arg Trp Val Glu Cys Arg Arg Asn Gly Leu Arg Asn Ile His Arg
 675 680 685
 Phe Ser Trp Pro His His Cys Arg Leu Tyr Leu Ser His Val Ser Thr
 690 695 700
 Tyr Cys Asp Gln Pro Ser Pro His Gln Pro Leu Arg Val Pro Leu Ala
 705 710 715 720
 Leu Gly Ser Ser Thr Ser Phe Gly Ala Asp Asp Ser Leu Ser Asp Ser
 725 730 735
 Leu Arg Gly Leu Ser Leu Gln Ile Ser Val Asp Ala Ser Ser Asp Leu
 740 745 750
 Asn Ala Ala Asp Ser Ala Ala Ala Ile Met Asp Ala Leu Arg Arg Arg
 755 760 765
 Pro Ala Ser Glu Lys Pro Ala Ser Ser Gly Ala Arg Ala Leu Gly Phe
 770 775 780
 Ala Pro Gly Arg Arg Glu Ser Leu Leu Val Val Ala Val Asp Cys Tyr
 785 790 795 800
 Gly Asp Asp Gly Lys Pro Asp Val Glu Gln Leu Lys Lys Ala Ile Asp
 805 810 815
 Ala Ala Val Ser Val Gly Glu Cys Ala Gly Ala Lys Gln Gly Tyr Val
 820 825 830
 Leu Ser Thr Gly Met Thr Ile Pro Glu Ala Ala Glu Ala Ile Lys Ala
 835 840 845
 Cys Gly Ala Asp Val Ala Ser Phe Asp Ala Leu Ile Cys Ser Ser Gly
 850 855 860
 Ala Glu Leu Cys Tyr Pro Trp Lys Lys Leu Val Ala Asp Glu Glu Tyr
 865 870 875 880
 Ser Gly His Val Ala Phe Arg Trp Pro Gly Asp His Val Lys Ser Ala
 885 890 895
 Val Pro Arg Leu Gly Ser Met Glu Glu Ile Ala Leu Ala Ile Asp Arg
 900 905 910

Pro Ala Ser Ser Val His Cys His Ala Tyr Ala Ala Thr Asp Ala Ser
 915 920 925
 Lys Val Ser Ile Thr Glu His Tyr Leu
 930 935

<210> 74
 <211> 808
 <212> PRT
 <213> Lolium perenne

<400> 74
 Met Ala Ala Lys Leu Thr Arg Leu His Ser Leu Arg Glu Arg Leu Gly
 1 5 10 15
 Ala Thr Phe Ser Ser His Pro Asn Glu Leu Ile Ala Leu Phe Ser Lys
 20 25 30
 Tyr Val His Gln Gly Lys Gly Met Leu Gln Arg His Gln Leu Leu Thr
 35 40 45
 Glu Phe Glu Ala Leu Phe Glu Ala Asp Lys Glu Arg Tyr Ala Pro Phe
 50 55 60
 Glu Asp Ile Leu Arg Ala Ala Gln Glu Ala Ile Val Leu Pro Pro Trp
 65 70 75 80
 Val Ala Leu Ala Ile Arg Pro Arg Pro Gly Val Trp Asp Tyr Ile Arg
 85 90 95
 Val Asn Val Ser Glu Leu Ala Val Glu Glu Leu Thr Val Ser Glu Tyr
 100 105 110
 Leu Ala Phe Lys Glu Gln Leu Val Asp Glu His Ala Ser Ser Lys Phe
 115 120 125
 Val Leu Glu Leu Asp Phe Glu Pro Phe Asn Ala Ser Phe Pro Arg Pro
 130 135 140
 Ser Met Ser Lys Ser Ile Gly Asn Gly Val Gln Phe Leu Asn Arg His
 145 150 155 160
 Leu Ser Ser Lys Leu Phe Gln Asp Lys Glu Ser Leu Tyr Pro Leu Leu
 165 170 175
 Asn Phe Leu Lys Ala His Asn His Gln Gly Thr Thr Met Met Leu Asn
 180 185 190
 Asp Arg Ile Gln Ser Leu Arg Gly Leu Gln Ser Ala Leu Arg Lys Ala
 195 200 205
 Glu Glu Tyr Leu Thr Ser Ile Pro Glu Asp Thr Pro Ser Ser Glu Phe
 210 215 220
 Asn His Arg Phe Gln Glu Leu Gly Leu Glu Lys Gly Trp Gly Asp Thr
 225 230 235 240
 Ala Lys Arg Val Gln Asp Thr Ile His Leu Leu Leu Asp Leu Leu Glu
 245 250 255
 Ala Pro Asp Pro Ala Ser Leu Glu Lys Phe Leu Gly Thr Ile Pro Met
 260 265 270
 Met Phe Asn Val Val Ile Leu Ser Pro His Gly Tyr Phe Ala Gln Ser
 275 280 285
 Asn Val Leu Gly Tyr Pro Asp Thr Gly Gly Gln Val Val Tyr Ile Leu
 290 295 300
 Asp Gln Val Arg Ala Leu Glu Asn Glu Met Leu Leu Arg Ile Lys Gln
 305 310 315 320
 Gln Gly Leu Asp Ile Thr Pro Lys Ile Leu Ile Val Thr Arg Leu Leu
 325 330 335
 Pro Asp Ala Val Gly Thr Thr Cys Gly Gln Arg Leu Glu Lys Val Ile
 340 345 350
 Gly Thr Glu His Thr Asp Ile Leu Arg Val Pro Phe Arg Thr Glu Lys
 355 360 365
 Gly Ile Leu Arg Lys Trp Ile Ser Arg Phe Asp Val Trp Pro Tyr Leu
 370 375 380
 Glu Thr Tyr Thr Glu Asp Val Ala Asn Glu Leu Met Arg Glu Met Gln
 385 390 395 400
 Thr Lys Pro Asp Leu Ile Ile Gly Asn Tyr Ser Asp Gly Asn Leu Val
 405 410 415
 Ala Thr Leu Leu Ala His Lys Leu Gly Val Thr Gln Cys Thr Ile Ala
 420 425 430

His Ala Leu Glu Lys Thr Lys Tyr Pro Asn Ser Asp Ile Tyr Leu Asp
 435 440 445
 Lys Phe Asp Ser Gln Tyr His Phe Ser Cys Gln Phe Thr Ala Asp Leu
 450 455 460
 Ile Ala Met Asn His Thr Asp Phe Ile Ile Thr Ser Thr Phe Gln Glu
 465 470 475 480
 Ile Ala Gly Ser Lys Asp Ser Val Gly Gln Tyr Glu Ser His Ile Ala
 485 490 495
 Phe Thr Leu Pro Asp Leu Tyr Arg Val Val His Gly Ile Asp Val Phe
 500 505 510
 Asp Pro Lys Phe Asn Ile Val Ser Pro Gly Ala Asp Met Thr Val Tyr
 515 520 525
 Phe Pro Tyr Thr Glu Thr Asp Lys Arg Leu Thr Ala Phe His Pro Glu
 530 535 540
 Ile Glu Glu Leu Leu Tyr Ser Asp Val Glu Asn Ser Glu His Lys Phe
 545 550 555 560
 Val Leu Lys Asp Lys Asn Lys Pro Ile Ile Phe Ser Met Ala Arg Leu
 565 570 575
 Asp Arg Val Lys Asn Met Thr Gly Leu Val Glu Met Phe Gly Lys Asn
 580 585 590
 Ala His Leu Lys Asp Leu Ala Asn Leu Val Ile Val Ala Gly Asp His
 595 600 605
 Gly Lys Glu Ser Lys Asp Arg Glu Glu Gln Ala Glu Phe Lys Arg Met
 610 615 620
 Tyr Ser Leu Ile Glu Glu Tyr Lys Leu Glu Gly His Ile Arg Trp Ile
 625 630 635 640
 Ser Ala Gln Met Asn Arg Val Arg Asn Ala Glu Leu Tyr Arg Tyr Ile
 645 650 655
 Cys Asp Thr Lys Gly Ala Phe Val Gln Pro Ala Phe Tyr Glu Ala Phe
 660 665 670
 Gly Leu Thr Val Val Glu Ala Met Thr Cys Gly Leu Pro Thr Ile Ala
 675 680 685
 Thr Cys His Gly Gly Pro Ala Glu Ile Ile Val Asn Gly Val Ser Gly
 690 695 700
 Leu His Ile Asp Pro Tyr His Ser Asp Lys Ala Ala Asp Ile Leu Val
 705 710 715 720
 Asn Phe Phe Glu Lys Ser Thr Ala Asp Pro Thr Tyr Trp Asp Lys Met
 725 730 735
 Ser Glu Gly Gly Leu Lys Arg Ile Tyr Glu Lys Tyr Thr Trp Lys Leu
 740 745 750
 Tyr Ser Glu Arg Leu Met Thr Leu Thr Gly Val Tyr Gly Phe Trp Lys
 755 760 765
 Tyr Val Ser Asn Leu Glu Arg Arg Glu Thr Arg Arg Tyr Leu Glu Met
 770 775 780
 Phe Tyr Ala Leu Lys Tyr Arg Ser Leu Ala Ala Val Pro Leu Ala
 785 790 795 800
 Val Asp Gly Glu Asn Thr Asp Asn
 805

<210> 75

<211> 808

<212> PRT

<213> Festuca arundinacea

<400> 75

Met Ala Ala Lys Leu Thr Arg Leu His Ser Leu Arg Glu Arg Leu Gly
 1 5 10 15
 Ala Thr Phe Ser Ser His Pro Asn Glu Leu Ile Ala Leu Phe Ser Lys
 20 25 30
 Tyr Val His Gln Gly Lys Gly Met Leu Gln Arg His Gln Leu Leu Thr
 35 40 45
 Glu Phe Glu Ala Leu Phe Glu Ser Asp Lys Glu Arg Tyr Ala Pro Phe
 50 55 60
 Gln Asp Ile Leu Arg Ala Ala Gln Glu Ala Ile Val Leu Pro Pro Trp
 65 70 75 80

Val	Ala	Leu	Ala	Ile	Arg	Pro	Arg	Pro	Gly	Val	Trp	Asp	Tyr	Ile	Arg
				85					90					95	
Val	Asn	Val	Ser	Glu	Leu	Ala	Val	Glu	Glu	Leu	Thr	Val	Ser	Glu	Tyr
			100					105					110		
Leu	Ala	Phe	Lys	Glu	Gln	Leu	Val	Asp	Glu	His	Ala	Ser	Ser	Lys	Phe
		115					120					125			
Val	Leu	Glu	Leu	Asp	Phe	Glu	Pro	Phe	Asn	Ala	Ser	Phe	Pro	Arg	Pro
	130					135					140				
Ser	Met	Ser	Lys	Ser	Ile	Gly	Asn	Gly	Val	Gln	Phe	Leu	Asn	Arg	His
145					150					155				160	
Leu	Ser	Ser	Lys	Leu	Phe	Gln	Asp	Lys	Glu	Ser	Leu	Tyr	Pro	Leu	Leu
			165						170					175	
Asn	Phe	Leu	Lys	Ala	His	Asn	His	Lys	Gly	Thr	Thr	Met	Met	Leu	Asn
			180					185					190		
Asp	Arg	Ile	Thr	Ser	Leu	Arg	Gly	Leu	Gln	Ser	Ala	Leu	Arg	Lys	Ala
		195					200					205			
Glu	Glu	Tyr	Leu	Thr	Ser	Ile	Leu	Glu	Asp	Thr	Pro	Ser	Phe	Glu	Phe
	210					215					220				
Asn	His	Arg	Phe	Gln	Glu	Leu	Gly	Leu	Glu	Lys	Gly	Trp	Gly	Asp	Thr
225					230					235				240	
Ala	Lys	Arg	Val	Gln	Asp	Thr	Ile	His	Leu	Leu	Leu	Asp	Leu	Leu	Glu
			245						250					255	
Ala	Pro	Asp	Pro	Ala	Ser	Leu	Glu	Lys	Phe	Leu	Gly	Thr	Ile	Pro	Met
			260					265					270		
Met	Phe	Asn	Val	Val	Ile	Leu	Ser	Pro	His	Gly	Tyr	Phe	Ala	Gln	Ser
		275					280					285			
Asn	Val	Leu	Gly	Tyr	Pro	Asp	Thr	Gly	Gly	Gln	Val	Val	Tyr	Ile	Leu
	290					295					300				
Asp	Gln	Val	Arg	Ala	Leu	Glu	Asn	Glu	Met	Leu	Leu	Arg	Ile	Lys	Gln
305					310					315				320	
Gln	Gly	Leu	Asp	Ile	Thr	Pro	Lys	Ile	Leu	Ile	Val	Thr	Arg	Leu	Leu
			325						330					335	
Pro	Asp	Ala	Val	Gly	Thr	Thr	Cys	Gly	Gln	Arg	Leu	Glu	Lys	Val	Ile
		340						345					350		
Gly	Thr	Glu	His	Thr	Asp	Ile	Leu	Arg	Val	Pro	Phe	Arg	Thr	Glu	Lys
		355					360					365			
Gly	Ile	Leu	Arg	Lys	Trp	Ile	Ser	Arg	Phe	Asp	Val	Trp	Pro	Tyr	Leu
	370					375					380				
Glu	Thr	Tyr	Thr	Glu	Asp	Val	Ala	Asn	Glu	Leu	Met	Arg	Glu	Met	Gln
385					390					395				400	
Thr	Lys	Pro	Asp	Leu	Ile	Ile	Gly	Asn	Tyr	Ser	Asp	Gly	Asn	Leu	Val
			405						410					415	
Ala	Thr	Leu	Leu	Ala	His	Lys	Leu	Gly	Val	Thr	Gln	Cys	Thr	Ile	Ala
		420						425					430		
His	Ala	Leu	Glu	Lys	Thr	Lys	Tyr	Pro	Asn	Ser	Asp	Ile	Tyr	Leu	Asp
		435					440					445			
Lys	Phe	Asp	Ser	Gln	Tyr	His	Phe	Ser	Cys	Gln	Phe	Thr	Ala	Asp	Leu
	450					455					460				
Ile	Ala	Met	Asn	His	Thr	Asp	Phe	Ile	Ile	Thr	Ser	Thr	Phe	Gln	Glu
465					470					475				480	
Ile	Ala	Gly	Ser	Lys	Asp	Ser	Val	Gly	Gln	Tyr	Glu	Ser	His	Ile	Ala
			485						490					495	
Phe	Thr	Leu	Pro	Asp	Leu	Tyr	Arg	Val	Val	His	Gly	Ile	Asp	Val	Phe
		500						505					510		
Asp	Pro	Lys	Phe	Asn	Ile	Val	Ser	Pro	Gly	Ala	Asp	Met	Ser	Val	Tyr
		515					520					525			
Phe	Pro	Tyr	Thr	Glu	Thr	Asp	Lys	Arg	Leu	Thr	Ala	Phe	His	Pro	Glu
	530					535					540				
Ile	Glu	Glu	Leu	Leu	Tyr	Ser	Asp	Val	Glu	Asn	Ser	Glu	His	Lys	Phe
545					550					555				560	
Val	Leu	Lys	Asp	Lys	Asn	Lys	Pro	Ile	Ile	Phe	Ser	Met	Ala	Arg	Leu
			565						570					575	
Asp	Arg	Val	Lys	Asn	Met	Thr	Gly	Leu	Val	Glu	Met	Phe	Gly	Lys	Asn
		580						585					590		
Ala	His	Leu	Lys	Asp	Leu	Ala	Asn	Leu	Val	Ile	Val	Ala	Gly	Asp	His
		595					600						605		

Gly Lys Glu Ser Lys Asp Arg Glu Glu Gln Ala Glu Phe Lys Arg Met
 610 615 620
 Tyr Ser Leu Ile Glu Glu Tyr Lys Leu Lys Gly His Ile Arg Trp Ile
 625 630 635 640
 Ser Ala Gln Met Asn Arg Val Arg Asn Ala Glu Leu Tyr Arg Tyr Ile
 645 650 655
 Cys Asp Thr Lys Gly Ala Phe Val Gln Pro Ala Phe Tyr Glu Ala Phe
 660 665 670
 Gly Leu Thr Val Ile Glu Ala Met Thr Cys Gly Leu Pro Thr Ile Ala
 675 680 685
 Thr Cys His Gly Gly Pro Ala Glu Ile Ile Val Asp Gly Val Ser Gly
 690 695 700
 Leu His Ile Asp Pro Tyr His Ser Asp Lys Ala Ala Asp Ile Leu Val
 705 710 715 720
 Asn Phe Phe Glu Lys Ser Thr Ala Asp Pro Thr Tyr Trp Asp Lys Met
 725 730 735
 Ser Glu Gly Gly Leu Lys Arg Ile Tyr Glu Lys Tyr Thr Trp Lys Leu
 740 745 750
 Tyr Ser Glu Arg Leu Met Thr Leu Thr Gly Val Tyr Gly Phe Trp Lys
 755 760 765
 Tyr Val Ser Asn Leu Glu Arg Arg Glu Thr Arg Arg Tyr Leu Glu Met
 770 775 780
 Phe Tyr Ala Leu Lys Tyr Arg Ser Leu Ala Ala Ala Val Pro Leu Ala
 785 790 795 800
 Val Asp Gly Glu Asn Thr Asp Ser
 805

<210> 76

<211> 814

<212> PRT

<213> Lolium perenne

<400> 76

Met Gly Glu Ala Ala Gly Asp Arg Val Leu Ser Arg Leu His Ser Val
 1 5 10 15
 Arg Glu Arg Ile Gly Asp Ser Leu Ser Ala His Pro Asn Glu Leu Val
 20 25 30
 Ala Val Phe Thr Arg Leu Val Asn Leu Gly Lys Gly Met Leu Gln Pro
 35 40 45
 His Gln Ile Ile Ala Glu Tyr Asn Thr Ala Ile Pro Glu Ala Glu Arg
 50 55 60
 Glu Lys Leu Lys Asp Gly Ala Phe Glu Asp Val Leu Arg Ala Ala Gln
 65 70 75 80
 Glu Ala Ile Val Ile Ser Pro Trp Val Ala Leu Ala Ile Arg Pro Arg
 85 90 95
 Pro Gly Val Trp Glu Tyr Val Arg Val Asn Val Ser Glu Leu Ala Val
 100 105 110
 Glu Glu Leu Ser Val Pro Glu Tyr Leu Gln Phe Lys Glu Gln Leu Val
 115 120 125
 Glu Gly Ser Asn Lys Asp Phe Val Leu Glu Leu Asp Phe Glu Pro Phe
 130 135 140
 Asn Ala Ser Phe Pro Arg Pro Ser Leu Ser Lys Ser Ile Gly Asn Gly
 145 150 155 160
 Val Gln Phe Leu Asn Arg His Leu Ser Ser Lys Leu Phe His Asp Lys
 165 170 175
 Glu Ser Met Tyr Pro Leu Leu Asn Phe Leu Arg Ala His Asn Tyr Lys
 180 185 190
 Gly Met Pro Met Met Met Asn Asp Arg Val Arg Ser Leu Ser Ala Leu
 195 200 205
 Gln Gly Ala Leu Arg Lys Ala Glu Glu His Leu Ser Gly Leu Pro Ala
 210 215 220
 Asp Thr Pro Tyr Ser Asp Phe His His Arg Phe Gln Glu Leu Gly Leu
 225 230 235 240
 Glu Lys Gly Trp Gly Asp Cys Ala Lys Arg Ala Gln Glu Thr Leu His
 245 250 255

Leu Leu Leu Asp Leu Leu Glu Ala Pro Asp Pro Ser Thr Leu Glu Lys
 260 265 270
 Phe Leu Gly Thr Ile Pro Met Val Phe Asn Val Val Ile Leu Ser Pro
 275 280 285
 His Gly Tyr Phe Ala Gln Ala Asn Val Leu Gly Tyr Pro Asp Thr Gly
 290 295 300
 Gly Gln Val Val Tyr Ile Leu Asp Gln Val Arg Ala Met Glu Asn Glu
 305 310 315 320
 Met Leu Leu Arg Ile Lys Gln Gln Gly Leu Asp Ile Thr Pro Arg Ile
 325 330 335
 Leu Ile Val Thr Arg Leu Leu Pro Asp Ala Thr Gly Thr Thr Cys Gly
 340 345 350
 Gln Arg Leu Glu Lys Val Leu Gly Thr Glu His Thr His Ile Leu Arg
 355 360 365
 Val Pro Phe Arg Thr Glu Asn Gly Ile Val Arg Lys Trp Ile Ser Arg
 370 375 380
 Phe Glu Val Trp Pro Tyr Leu Glu Thr Phe Thr Asp Asp Val Ala His
 385 390 395 400
 Glu Ile Ser Gly Glu Leu Gln Ala Asn Pro Asp Leu Ile Ile Gly Asn
 405 410 415
 Tyr Ser Asp Gly Asn Leu Val Ala Cys Leu Leu Ala His Lys Met Gly
 420 425 430
 Val Thr His Cys Thr Ile Ala His Ala Leu Glu Lys Thr Lys Tyr Pro
 435 440 445
 Asn Ser Asp Leu Tyr Trp Lys Lys Phe Glu Asp His Tyr His Phe Ser
 450 455 460
 Cys Gln Phe Thr Thr Asp Leu Ile Ala Met Asn His Ala Asp Phe Ile
 465 470 475 480
 Ile Thr Ser Thr Phe Gln Glu Ile Ala Gly Asn Lys Asp Thr Val Gly
 485 490 495
 Gln Tyr Glu Ser His Met Ala Phe Thr Met Pro Gly Met Tyr Arg Val
 500 505 510
 Val His Gly Ile Asp Val Phe Asp Pro Lys Phe Asn Ile Val Ser Pro
 515 520 525
 Gly Ala Asp Met Ser Ile Tyr Phe Pro Tyr Ser Glu Ser Gln Arg Arg
 530 535 540
 Leu Thr Ser Leu His Pro Glu Ile Glu Glu Leu Leu Tyr Ser Asp Val
 545 550 555 560
 Asp Asn Asp Glu His Ser Cys Leu Lys Asp Arg Asn Lys Pro Ile Ile
 565 570 575
 Phe Ser Met Ala Arg Leu Asp Arg Val Lys Asn Leu Thr Gly Leu Val
 580 585 590
 Glu Leu Tyr Gly Arg Asn Pro Arg Leu Gln Glu Leu Val Asn Leu Val
 595 600 605
 Val Val Cys Gly Asp His Gly Asn Pro Ser Lys Asp Lys Glu Glu Gln
 610 615 620
 Ala Glu Phe Lys Lys Met Phe Asp Leu Ile Glu Gln Tyr Asn Leu Asn
 625 630 635 640
 Gly His Ile Arg Trp Ile Ser Ala Gln Met Asn Arg Val Arg Asn Ala
 645 650 655
 Glu Leu Tyr Arg Tyr Ile Cys Asp Thr Lys Gly Ala Phe Val Gln Pro
 660 665 670
 Ala Phe Tyr Glu Ala Phe Gly Leu Thr Val Ile Glu Ala Met Thr Cys
 675 680 685
 Gly Leu Pro Thr Phe Ala Thr Ala Tyr Gly Gly Pro Ala Glu Ile Ile
 690 695 700
 Val Asn Gly Val Ser Gly Tyr His Ile Asp Pro Tyr Gln Gly Asp Lys
 705 710 715 720
 Ala Ser Ala Leu Leu Val Glu Phe Phe Glu Lys Cys Gln Gly Asp His
 725 730 735
 Ser His Trp Thr Lys Ile Ser Leu Gly Gly Leu Gln Arg Ile Glu Glu
 740 745 750
 Lys Tyr Thr Trp Lys Leu Tyr Ser Glu Arg Leu Met Thr Leu Thr Gly
 755 760 765
 Val Tyr Gly Phe Trp Lys Tyr Val Ser Asn Leu Glu Arg Arg Glu Thr
 770 775 780

Arg Arg Tyr Leu Glu Met Leu Tyr Ala Leu Lys Tyr Arg Thr Met Ala
 785 790 795 800
 Ser Thr Val Pro Leu Ala Val Glu Gly Glu Pro Ser Ser Lys
 805 810

<210> 77

<211> 816

<212> PRT

<213> Festuca arundinacea

<400> 77

Met Gly Glu Ser Ala Gly Glu Arg Ala Leu Ser Arg Leu His Ser Val
 1 5 10 15
 Arg Glu Arg Ile Gly Asp Ser Leu Ser Ala His Thr Asn Glu Leu Val
 20 25 30
 Ala Val Phe Ser Arg Leu Val Asn His Gly Lys Gly Met Leu Gln Pro
 35 40 45
 His Gln Ile Thr Ala Glu Tyr Asn Ala Ala Ile Pro Glu Ala Glu Arg
 50 55 60
 Glu Lys Leu Lys Asp Thr Ala Phe Glu Asp Leu Leu Arg Gly Ala Gln
 65 70 75 80
 Glu Ala Ile Val Ile Pro Pro Trp Val Ala Leu Ala Ile Arg Pro Arg
 85 90 95
 Pro Gly Val Trp Glu Tyr Val Arg Val Asn Val Ser Glu Leu Gly Val
 100 105 110
 Glu Glu Leu Ser Val Pro Glu Tyr Leu Gln Phe Lys Glu Gln Leu Val
 115 120 125
 Asn Glu Ser Thr Asp Asn Asn Phe Val Leu Glu Leu Asp Phe Gly Pro
 130 135 140
 Phe Asn Ala Ser Phe Pro Arg Pro Ser Leu Ser Lys Ser Ile Gly Asn
 145 150 155 160
 Gly Val Gln Phe Leu Asn Arg His Leu Ser Ser Lys Leu Phe His Asp
 165 170 175
 Lys Glu Ser Met Tyr Pro Leu Leu Asn Phe Leu Arg Ala His Asn Tyr
 180 185 190
 Lys Gly Met Thr Met Met Leu Asn Asp Arg Ile Arg Ser Leu Ser Ala
 195 200 205
 Leu Gln Asp Ala Leu Arg Lys Ala Glu Lys His Leu Ser Gly Leu Pro
 210 215 220
 Ala Asp Thr Pro Tyr Ser Glu Phe His His Arg Phe Gln Glu Leu Gly
 225 230 235 240
 Leu Glu Lys Gly Trp Gly Asp Cys Thr Gln Arg Ala His Glu Thr Ile
 245 250 255
 His Leu Leu Leu Asp Leu Leu Glu Ala Pro Asp Pro Ser Thr Leu Glu
 260 265 270
 Lys Phe Leu Gly Thr Ile Pro Met Val Phe Asn Val Val Ile Leu Ser
 275 280 285
 Pro His Gly Tyr Phe Ala Gln Ala Asn Val Leu Gly Tyr Pro Asp Thr
 290 295 300
 Gly Gly Gln Val Val Tyr Ile Leu Asp Gln Val Arg Ala Met Glu Asn
 305 310 315 320
 Glu Met Leu Leu Arg Ile Lys Gln Gln Gly Leu Asp Ile Thr Pro Lys
 325 330 335
 Ile Leu Ile Val Thr Arg Leu Leu Pro Asp Ala His Gly Thr Thr Cys
 340 345 350
 Gly Gln Arg Leu Glu Lys Val Leu Gly Thr Glu His Thr His Ile Leu
 355 360 365
 Arg Val Pro Phe Lys Thr Glu Asp Gly Ile Val Arg Lys Trp Ile Ser
 370 375 380
 Arg Phe Glu Val Trp Pro Tyr Leu Glu Ala Tyr Thr Asp Asp Val Ala
 385 390 395 400
 His Glu Ile Ala Gly Glu Leu Gln Ala Asn Pro Asp Leu Ile Ile Gly
 405 410 415
 Asn Tyr Ser Asp Gly Asn Leu Val Ala Cys Leu Leu Ala His Lys Leu
 420 425 430

Gly Val Thr His Cys Thr Ile Ala His Ala Leu Glu Lys Thr Lys Tyr
 435 440 445
 Pro Asn Ser Asp Leu Tyr Trp Lys Lys Phe Glu Asp His Tyr His Phe
 450 455 460
 Ser Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn His Ala Asp Phe
 465 470 475 480
 Ile Ile Thr Ser Thr Phe Gln Glu Ile Ala Gly Asn Lys Asp Thr Val
 485 490 495
 Gly Gln Tyr Glu Ser His Met Ala Phe Thr Met Pro Gly Leu Tyr Arg
 500 505 510
 Val Val His Gly Ile Asp Val Phe Asp Pro Lys Phe Asn Ile Val Ser
 515 520 525
 Pro Gly Ala Asp Met Thr Ile Tyr Phe Pro Tyr Thr Glu Gln Gln Lys
 530 535 540
 Arg Leu Thr Ser Leu His Ala Glu Ile Glu Glu Leu Leu Phe Ser Asp
 545 550 555 560
 Val Glu Asn Ser Glu His Lys Phe Val Leu Lys Asp Lys Asn Lys Pro
 565 570 575
 Ile Ile Phe Ser Met Ala Arg Leu Asp Arg Val Lys Asn Met Thr Gly
 580 585 590
 Leu Val Glu Leu Tyr Gly Arg Asn Pro Arg Leu Gln Glu Leu Val Asn
 595 600 605
 Leu Val Val Val Cys Gly Asp His Gly Lys Glu Ser Lys Asp Lys Glu
 610 615 620
 Glu Gln Ala Glu Phe Lys Arg Met Phe Asp Leu Ile Glu Gln Tyr Asn
 625 630 635 640
 Leu Ser Ser His Ile Arg Trp Ile Ser Ala Gln Met Asn Arg Val Arg
 645 650 655
 Asn Gly Glu Leu Tyr Arg Tyr Ile Cys Asp Met Lys Gly Ala Phe Val
 660 665 670
 Gln Pro Ala Phe Tyr Glu Ala Phe Gly Leu Thr Val Ile Glu Ala Met
 675 680 685
 Thr Cys Gly Leu Pro Thr Phe Ala Thr Ala Tyr Gly Gly Pro Ala Glu
 690 695 700
 Ile Ile Val Asn Gly Val Ser Gly Tyr His Ile Asp Pro Tyr Gln Asn
 705 710 715 720
 Asp Lys Ala Ser Ala Leu Leu Val Glu Phe Glu Lys Cys Gln Glu
 725 730 735
 Asp Pro Ser His Trp Asn Lys Ile Ser Gln Gly Gly Leu Gln Arg Ile
 740 745 750
 Glu Glu Lys Tyr Thr Trp Lys Leu Tyr Ser Glu Arg Leu Met Thr Leu
 755 760 765
 Ser Gly Val Tyr Gly Phe Trp Lys Tyr Val Ser Asn Leu Asp Arg Arg
 770 775 780
 Glu Thr Arg Arg Tyr Leu Glu Met Leu Tyr Ala Leu Lys Tyr Arg Lys
 785 790 795 800
 Met Ala Thr Thr Val Pro Leu Ala Ile Glu Gly Glu Thr Thr Gly Lys
 805 810 815

<210> 78

<211> 478

<212> PRT

<213> Festuca arundinacea

<400> 78

Trp Ile Ile Leu Glu Pro Ala Ile Glu Pro Asp Thr Pro Gly Asp Ile
 1 5 10 15
 Lys Gly Cys Trp Ser Ala Ser Ala Thr Val Ile Ser Gly Ser Gln Pro
 20 25 30
 Val Ile Met Tyr Thr Gly Gly Asp Val Glu Asn His Gln Val Gln Asn
 35 40 45
 Ile Ala Leu Pro Lys Asn Arg Ser Asp Pro Tyr Leu Ile Glu Trp Thr
 50 55 60
 Lys Ala Cys Asn Asn Pro Val Leu Gln Pro Val Gly Pro Gly Met Asn
 65 70 75 80

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Pro Gly Glu Phe Arg Asp Pro Thr Thr Gly Trp Ile Gly Pro Asp Gly
      85      90      95
Leu Trp Arg Ile Ser Ile Gly Ala Glu Val Asn Gly Tyr Ser Ala Ala
      100      105      110
Leu Leu Tyr Lys Ser Glu Asp Phe Leu Asn Trp Ser Arg Val Asp His
      115      120      125
Pro Leu Tyr Ser Ser Ser Ala Ser Thr Met Trp Glu Cys Leu Asp Phe
      130      135      140
Phe Ala Val Leu Pro Gly Ser Asn Gly Gly Leu Asp Leu Ser Ala Ala
      145      150      155      160
Ile Pro Lys Gly Ala Lys His Val Leu Lys Val Ser Val Asp Gln Cys
      165      170      175
Asp Lys Tyr Met Ile Gly Val Tyr Asp Leu Glu His Asp Ala Phe Val
      180      185      190
Pro Asp Thr Ile Leu Asp Asp Arg Trp Leu Leu Pro Arg Ile Asp Tyr
      195      200      205
Gly Asn Tyr Tyr Ala Ser Lys Ser Phe Phe Asp Ser Lys Asn Arg Arg
      210      215      220
Arg Ile Ile Trp Gly Trp Thr Asn Glu Ser Asp Ser Ser Ser Asp Asp
      225      230      235      240
Val Ala Lys Gly Trp Ala Gly Ile Tyr Ala Ile Pro Arg Thr Ile Trp
      245      250      255
Leu Asp Arg Asp Gly Lys Gln Leu Leu Gln Trp Pro Val Glu Glu Ile
      260      265      270
Glu Ser Leu Arg Arg Asn Glu Ile Asn Tyr Gln Gly Leu Asp Leu Glu
      275      280      285
Lys Gly Asp Leu Tyr Glu Ile Lys Gly Val Asp Thr Leu Gln Ala Asp
      290      295      300
Val Glu Ile Asp Phe Glu Leu Thr Ser Ile Asp Asp Ala Asp Ser Phe
      305      310      315      320
Asp Pro Ser Trp Leu Leu Asp Pro Glu Lys His Cys Arg Glu Ala Gly
      325      330      335
Ala Ser Val His Gly Gly Ile Gly Pro Phe Gly Leu Val Ile Leu Ala
      340      345      350
Thr Gly Asp Met Glu Glu His Thr Val Val His Phe Arg Val Tyr Lys
      355      360      365
Ser Gln Lys Glu Tyr Met Ile Leu Met Cys Ser Asp Ile Arg Arg Ser
      370      375      380
Ser Leu Arg Gln Gly Leu Tyr Ala Pro Ala Tyr Gly Gly Phe Phe Glu
      385      390      395      400
Phe Asp Leu Glu Lys Glu Arg Lys Ile Ser Leu Arg Thr Leu Ile Asp
      405      410      415
Arg Ser Ala Val Glu Ser Phe Gly Gly Gly Gly Arg Val Cys Ile Ile
      420      425      430
Ala Arg Val Tyr Pro Val Ala Ile Val Asp Asp Gly Ser Ala His Met
      435      440      445
Tyr Ala Phe Asn Asn Gly Ser Thr Thr Val Arg Val Pro Gln Ile Arg
      450      455      460
Ala Trp Ser Met Met Thr Ala Gln Val Asn Leu Lys Lys Gly
      465      470      475

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<210> 79

<211> 583

<212> PRT

<213> Lolium perenne

<400> 79

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Met Gly Asn Pro Lys Trp Val Leu Ala Pro Trp Ala Val Leu Leu Leu
  1      5      10      15
Leu Gln Leu Ala Ser Ala Ser His His Ala Arg Leu Ser Leu Glu Thr
      20      25      30
Ser Ala Ala Ser Pro Ser Val Pro Ala Ser Ile Val Ser Pro Leu Leu
      35      40      45
Arg Thr Gly Tyr His Phe Gln Pro Pro Met Asn Trp Ile Asn Asp Pro
      50      55      60

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Asn Gly Pro Leu Tyr Tyr Lys Gly Trp Tyr His Leu Phe Tyr Gln Tyr
65      70      75      80
Asn Pro Lys Gly Ala Val Trp Gly Asn Ile Ile Trp Ala His Ser Val
      85      90      95
Ser Arg Asp Leu Ile Asn Trp Ile Ala Leu Glu Pro Ala Ile Ser Pro
      100      105      110
Thr Ile Pro Thr Asp Gln Tyr Gly Val Trp Ser Gly Ser Thr Thr Ile
      115      120      125
Leu His Asp Gly Thr Pro Ala Ile Leu Tyr Thr Gly Ile Asp Arg Pro
      130      135      140
Ser Val Asn Tyr Gln Ile Gln Asn Ile Ala Leu Pro Lys Asn Ala Ser
145      150      155      160
Asp Pro Leu Leu Arg Glu Trp Tyr Lys Pro Gly Tyr Asn Pro Ile Ala
      165      170      175
Val Pro Val Glu Gly Ile Asn Ala Thr Gln Phe Arg Asp Pro Thr Thr
      180      185      190
Ala Trp Phe Ala Gly Arg His Trp Arg Met Leu Val Gly Gly Leu Arg
      195      200      205
Pro Gly Thr Leu Arg Gly Glu Ala Ile Leu Tyr Arg Ser Arg Asp Phe
      210      215      220
Lys His Trp Val Arg Ala Lys His Pro Leu His Ser Ala Leu Thr Gly
225      230      235      240
Met Trp Glu Cys Pro Asp Phe Phe Pro Val Gly Lys Ala Gly Val Glu
      245      250      255
Lys Gly Leu Asp Thr Ser Glu Tyr Gly Ala Ala Ala Gly Val Glu Lys
      260      265      270
His Val Leu Lys Asn Ser Leu Asp Leu Thr Arg Tyr Asp Tyr Tyr Thr
      275      280      285
Ile Gly Thr Tyr Asp Asn Val Lys Glu Arg Tyr Val Pro Asp Asn Pro
      290      295      300
Thr Gly Asp Val Tyr Gln Arg Leu Gln Tyr Asp Tyr Gly Asn Phe Tyr
305      310      315      320
Ala Ser Lys Thr Phe Phe Asp Pro Val Lys Gln Arg Arg Ile Leu Leu
      325      330      335
Gly Trp Ala Asn Glu Ser Asp Ser Val Ala His Asp Lys Ala Lys Gly
      340      345      350
Trp Ala Gly Ile Gln Ala Ile Pro Arg Lys Ile Trp Leu Asp Pro Ser
      355      360      365
Gly Lys Gln Leu Val Gln Trp Pro Val Glu Glu Leu Glu Lys Leu Arg
      370      375      380
Gly Lys Pro Val Asn Val Gly Asp Lys Val Val Lys Pro Gly Gln His
385      390      395      400
Phe Glu Val Thr Gly Leu Gln Ser Tyr Gln Ser Asp Val Glu Val Ser
      405      410      415
Phe Glu Val Ser Ser Leu Asp Lys Ala Glu Pro Phe Asp Pro Ala Tyr
      420      425      430
Ser Asn Asp Ala Gln Lys Leu Cys Gly Ile Lys Gly Ala Asp Val Lys
      435      440      445
Gly Gly Val Gly Pro Phe Gly Leu Trp Val Leu Ser Ser Ala Asp Leu
      450      455      460
Ala Glu Lys Thr Ala Val Phe Phe Arg Val Phe Lys Asp Gly Tyr Gly
465      470      475      480
Lys Pro Ile Val Leu Met Cys Ser Asp Pro Thr Lys Ser Ser Leu Thr
      485      490      495
Pro Asp Leu Tyr Lys Pro Thr Phe Ala Gly Phe Val Asp Thr Asp Ile
      500      505      510
Ser Ser Gly Lys Ile Ser Leu Arg Ser Leu Ile Asp Arg Ser Val Val
      515      520      525
Glu Ser Phe Gly Ala Gly Gly Lys Thr Cys Ile Leu Ser Arg Val Tyr
      530      535      540
Pro Ser Met Ala Leu Gly Lys Asp Ala His Leu His Val Phe Asn Asn
545      550      555      560
Gly Glu Thr Asp Ile Lys Val Ser Lys Leu Thr Ala Trp Glu Met Lys
      565      570      575
Arg Pro Leu Met Asn Gly Ala
      580

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<210> 80
 <211> 390
 <212> PRT
 <213> *Lolium perenne*

<400> 80
 Gly Val Gly Ser Leu Leu Val Tyr Arg Ser Ala Asp Phe Leu Arg Trp
 1 5 10 15
 Gln Arg Asn Ala Ala Pro Leu His Ala Ser Ser Arg Asp Val Pro Val
 20 25 30
 Leu Glu Cys Pro Asp Leu Phe Pro Val Ala Ala Ala Gln Gly Ala
 35 40 45
 Thr Glu Gly Leu Glu Thr Ser Ala Pro Ser Gly Ala Gly Val Arg His
 50 55 60
 Val Leu Lys Leu Thr Asp Phe Ala Lys Glu Asp His Tyr Met Val Gly
 65 70 75 80
 Phe Tyr Asp Asp Val Ala Asp Thr Phe Val Pro Ala Glu Pro Glu Arg
 85 90 95
 Gly Asp Asp Pro Asp Asn Trp Arg Arg Leu Asp His Gly His Leu Tyr
 100 105 110
 Ala Ser Lys Ser Phe Tyr Asp Ala Arg Asn Lys Arg Arg Ile Leu Trp
 115 120 125
 Ala Trp Val Asp Glu Thr Asp Gly Gly Gly Val Ala Arg Gly Trp Ala
 130 135 140
 Gly Ile Gln Ala Phe Pro Arg Ala Met Trp Leu Asp Ala Asp Gly Lys
 145 150 155 160
 Arg Leu Val Gln Trp Pro Val Glu Glu Ile Glu Thr Leu Arg Arg Lys
 165 170 175
 Arg Val Gly Leu Arg Trp Ala Thr Asp Val Glu Ala Gly Gly Arg Lys
 180 185 190
 Glu Ile Ala Gly Ile Val Ser Ser Gln Ala Asp Val Glu Val Val Phe
 195 200 205
 Glu Ile Pro Asn Leu Glu Glu Ala Glu Thr Leu Asp Pro Glu Trp Val
 210 215 220
 Leu Asp Pro Lys Gly Leu Cys Ala Ala Lys Gly Ala Ser Val His Gly
 225 230 235 240
 Gly Val Gly Pro Phe Gly Leu Leu Val Leu Ala Ser Gly Asp Leu Glu
 245 250 255
 Glu His Thr Ala Val Phe Phe Arg Val Phe Lys His Asp Gly Lys Tyr
 260 265 270
 Lys Val Leu Met Cys Thr Asp Leu Thr Lys Ser Ser Thr Lys Ala Gly
 275 280 285
 Ala His Lys Pro Ser Tyr Gly Ala Phe Leu Asp Val Asp Val Glu Lys
 290 295 300
 Asp Lys Phe Ile Ser Leu Arg Thr Leu Ile Asp His Thr Val Val Glu
 305 310 315 320
 Ser Phe Gly Asp Gly Gly Arg Thr Cys Met Thr Ala Arg Val Tyr Pro
 325 330 335
 Glu His Ala Ala Met Gly Ser Thr His Leu Tyr Val Phe Asn Asn Gly
 340 345 350
 Thr Gly Ala Val Lys Val Ser Lys Leu Glu Ala Trp Glu Leu Ala Thr
 355 360 365
 Ala Ala Val Asn Gly Gly Ser Leu Ala Pro Val Val Val Lys Ala Ser
 370 375 380
 Asp Pro Lys Glu Ala Leu
 385 390

<210> 81
 <211> 597
 <212> PRT
 <213> *Festuca arundinacea*

<400> 81
 Met Ala Gly Leu Arg Leu Ala Ala Cys Ala Ala Val Ala Val Leu Leu
 1 5 10 15

Cys Leu Leu Leu Ser Ser Ser Ala Ala Leu Arg Trp Leu Ser Asp Pro
 20 25 30
 Ala Pro Glu Ser Ala Ala Ala Gly Val Ser His Asp Ser Tyr Arg Thr
 35 40 45
 Ala Tyr His Phe Gln Pro Thr Glu Asn Trp Gln Asn Asp Pro Asn Gly
 50 55 60
 Pro Met Tyr Tyr Lys Gly Val Tyr His Phe Phe Tyr Gln Tyr Asn Pro
 65 70 75 80
 Tyr Arg Ala Thr Trp Gly Asn Gly Asn Leu Ser Trp Gly His Ser Val
 85 90 95
 Ser Val Asp Leu Val Asn Trp Ser Ala Leu Glu Asn Ala Met Asp Pro
 100 105 110
 Asp Ser Ser Phe Asp Ile Asn Gly Cys Trp Ser Gly Ser Ala Thr Ile
 115 120 125
 Leu Pro Asp Gly Thr Pro Val Phe Leu Tyr Thr Gly Ile Asp Ala Asp
 130 135 140
 Asn Asn Gln Val Gln Asn Val Ala Phe Pro Lys Asn Ala Ser Asp Pro
 145 150 155 160
 Leu Leu Arg Glu Trp Val Lys Pro Ser Tyr Asn Pro Val Ile Ala Leu
 165 170 175
 Pro Asp Asp Val Val His Asp Asn Phe Arg Asp Pro Ser Thr Ala Trp
 180 185 190
 Leu Gly Arg Asp Gly Leu Trp Arg Val Ala Val Ser Ala Gly Leu Lys
 195 200 205
 Asp Gly Thr Gly Thr Thr Leu Val Tyr Arg Ser Lys Asp Phe Arg Gln
 210 215 220
 Trp Glu Arg Asn Ala Glu Pro Leu Tyr Ser Ser Ser Asp Ala Gly Met
 225 230 235 240
 Val Glu Cys Pro Asp Leu Phe Pro Leu Ala Glu Pro Gly Asp Gln His
 245 250 255
 Gly Leu Asp Tyr Thr Pro Ser Asn Gly Ala Ala Val Ser Tyr Val Leu
 260 265 270
 Lys Gln Ser Val Met Asp Thr Leu Ser Asp Tyr Tyr Val Leu Gly Arg
 275 280 285
 Tyr Asp Asp Ala Ala Asp Thr Phe Ser Pro Val Glu Ala Asp Asn Asp
 290 295 300
 Cys Arg Thr Trp Gln Arg Phe Asp Tyr Gly His Val Tyr Ala Ser Lys
 305 310 315 320
 Ser Phe Tyr Asp Ala Gly Lys Lys Arg Arg Val Leu Trp Ser Trp Ala
 325 330 335
 Asn Glu Ser Asp Pro Glu Ala Asp Tyr Leu Ala Arg Gly Trp Ala Gly
 340 345 350
 Val Gln Ala Val Pro Arg Arg Ile Trp Leu Asp Ser Lys Gly Lys Gln
 355 360 365
 Leu Leu Gln Trp Pro Ile Glu Glu Ile Glu Thr Leu Arg Lys Thr Arg
 370 375 380
 Val Gly Leu Leu Gly Ala Glu Met Asn Ala Gly Gly Met Asn Glu Ile
 385 390 395 400
 Ile Gly Val Ala Gly Ala Gln Ala Asp Val Glu Val Val Phe Glu Val
 405 410 415
 Pro Ser Leu Glu Gly Ala Glu Asn Leu Asp Pro Asn Gln Leu Leu Asp
 420 425 430
 Pro Gln Arg Leu Cys Gly Glu Lys Gly Ala Ser Val Leu Gly Gly Val
 435 440 445
 Gly Pro Phe Gly Leu Leu Val Leu Ala Ser Gly Asp Leu Gln Glu His
 450 455 460
 Thr Ser Val Phe Phe Arg Val Phe Arg His Glu Gly Lys Tyr Lys Val
 465 470 475 480
 Leu Met Cys Thr Asp Leu Arg Arg Ser Thr Thr Arg Ala Asp Val Tyr
 485 490 495
 Lys Pro Pro Tyr Gly Gly Phe Val Asp Ile Asp Ile Glu Lys Glu Arg
 500 505 510
 Ser Ile Ser Leu Arg Thr Leu Val Asp His Ser Val Val Glu Ser Tyr
 515 520 525
 Gly Gly Gly Gly Arg Thr Val Ile Thr Ala Arg Val Tyr Pro Glu His
 530 535 540

Ala Ala Thr Thr Asn Ser Arg Leu Phe Met Phe Asn Asn Gly Thr Gly
 545 550 555 560
 Ala Val Lys Val Ser Lys Leu Asp Ala Trp Glu Leu Ala Pro Ala Lys
 565 570 575
 Val Asn Val Pro Gly Asp Gly Leu Ile Thr Ala Gly Ser Ser Met His
 580 585 590
 Leu Arg Glu Ala Tyr
 595

<210> 82

<211> 399

<212> PRT

<213> Festuca arundinacea

<400> 82

Leu Asn Ser Thr Glu Phe Arg Asp Pro Thr Thr Gly Trp Ile Gly Pro
 1 5 10 15
 Asp Gly Leu Trp Arg Ile Ala Ile Gly Ala Glu Leu Asn Gly Tyr Gly
 20 25 30
 Ala Ala Leu Leu Tyr Lys Ser Glu Asp Phe Leu Asn Trp Thr Arg Val
 35 40 45
 Asp His Pro Leu Tyr Ser Asp Asn Ala Pro Ser Met Trp Glu Cys Pro
 50 55 60
 Asp Phe Phe Ala Val Leu Pro Gly Asn Asn Gly Gly Leu Asp Leu Ser
 65 70 75 80
 Ala Ala Ile Pro Lys Gly Ala Lys His Val Leu Lys Met Ser Val Asp
 85 90 95
 Tyr Ser Asp Lys Tyr Met Ile Gly Val Tyr Asp Leu Lys Arg Asp Ala
 100 105 110
 Phe Val Pro Asp Val Val Leu Asp Asp Arg Arg Leu Trp Leu Arg Ile
 115 120 125
 Asp Tyr Gly Thr Phe Tyr Ala Ser Lys Ser Phe Phe Asp Ser Lys Arg
 130 135 140
 Gly Arg Arg Val Ile Trp Gly Trp Ser Asn Glu Thr Asp Ser Val Ser
 145 150 155 160
 Asp Asp Gly Ala Lys Gly Trp Ala Gly Ile His Ala Ile Pro Arg Ser
 165 170 175
 Ile Trp Leu Asp Ser Asp Gly Lys Gln Leu Leu Gln Trp Pro Ile Asp
 180 185 190
 Glu Ile Glu Ser Leu Arg Arg Asp Glu Ile Asn His Gln Gly Leu Glu
 195 200 205
 Leu Lys Asn Gly Asp Leu Phe Glu Ile Lys Gly Ile Asp Thr Leu Gln
 210 215 220
 Ala Asp Ile Glu Val Asp Phe Glu Leu Thr Ser Ile Asp Ser Ala Asp
 225 230 235 240
 Pro Phe Asp Pro Ser Trp Leu Leu Asp Val Glu Arg His Cys Arg Glu
 245 250 255
 Ala Gly Ala Ser Val Gln Gly Gly Ile Gly Pro Phe Gly Leu Val Val
 260 265 270
 Leu Ala Ser Asp Asn Met Glu Glu His Ile Ala Val His Phe Arg Val
 275 280 285
 Tyr Lys Ser Gln Lys Ser His Met Ile Leu Met Cys Ser Asp Leu Arg
 290 295 300
 Arg Ser Ser Leu Arg Ser Gly Leu Tyr Thr Pro Ala Tyr Gly Gly Phe
 305 310 315 320
 Phe Glu Phe Asp Leu Glu Lys Glu Arg Lys Ile Ser Leu Arg Thr Leu
 325 330 335
 Ile Asp Arg Ser Ala Val Glu Ser Phe Gly Gly Gly Gly Arg Val Cys
 340 345 350
 Ile Thr Ala Arg Ile Tyr Pro Val Ala Leu Val Asp Gly Arg Val His
 355 360 365
 Met Tyr Ala Phe Asn Asn Gly Ser Thr Thr Val Arg Val Pro Gln Leu
 370 375 380
 Gly Ala Trp Ser Met Met Thr Ala Gln Val Asn Val Asn Lys Gly
 385 390 395

<210> 83
 <211> 583
 <212> PRT
 <213> Festuca arundinacea

<400> 83
 Met Gly Asn Pro Lys Trp Ile Phe Ala Pro Trp Ala Val Leu Leu Leu
 1 5 10 15
 Phe Leu Leu Gln Leu Ala Cys Ala Ser His His Thr Arg Arg Ser Leu
 20 25 30
 Glu Thr Glu Ala Ala Ser Pro Ser Val Pro Ala Ser Ile Val Ser Pro
 35 40 45
 Leu Leu Arg Thr Gly Tyr His Phe Gln Pro Pro Met Asn Trp Ile Asn
 50 55 60
 Asp Pro Asn Gly Pro Leu Tyr Tyr Lys Gly Trp Tyr His Leu Phe Tyr
 65 70 75 80
 Gln Tyr Asn Pro Lys Gly Ala Val Trp Gly Asn Ile Ile Trp Ala His
 85 90 95
 Ser Val Ser Arg Asp Leu Ile Asn Trp Ile Ala Leu Glu Pro Ala Ile
 100 105 110
 Thr Pro Ser Ile Pro Thr Asp Lys Tyr Gly Val Trp Ser Gly Ser Thr
 115 120 125
 Thr Ile Leu His Asp Gly Thr Pro Ala Ile Leu Tyr Thr Gly Ile Asp
 130 135 140
 Arg Pro Ser Ile Asn Tyr Gln Ile Gln Asn Ile Ala Leu Pro Lys Asn
 145 150 155 160
 Ala Ser Asp Pro Leu Leu Arg Glu Trp Tyr Lys Pro Gly Tyr Asn Pro
 165 170 175
 Ile Ala Val Pro Val Ala Gly Met Asn Ala Thr Gln Phe Arg Asp Pro
 180 185 190
 Thr Thr Ala Trp Phe Ala Gly Arg His Trp Arg Met Leu Val Gly Gly
 195 200 205
 Leu Arg Pro Gly Thr Leu Arg Gly Glu Ala Ile Leu Tyr Arg Ser Leu
 210 215 220
 Asp Phe Lys Asn Trp Thr Arg Ala His His Pro Leu His Ser Ala Leu
 225 230 235 240
 Thr Gly Met Trp Glu Cys Pro Asp Phe Phe Pro Val Gly Glu Ala Gly
 245 250 255
 Val Glu Lys Gly Leu Asp Thr Ser Glu His Gly Glu Gly Val Glu Lys
 260 265 270
 His Val Leu Lys Asn Ser Leu Asp Leu Thr Arg Tyr Asp Tyr Tyr Thr
 275 280 285
 Val Gly Thr Tyr Asp Asn Val Lys Glu Arg Tyr Val Pro Asp Asn Pro
 290 295 300
 Thr Gly Asp Val Tyr Arg Arg Leu Gln Tyr Asp Tyr Gly Asn Phe Tyr
 305 310 315 320
 Ala Ser Lys Thr Phe Phe Asp Pro Val Lys Gln Arg Arg Ile Leu Leu
 325 330 335
 Gly Trp Ala Asn Glu Ser Asp Ser Val Ala His Asp Lys Ala Lys Gly
 340 345 350
 Trp Ala Gly Ile Gln Ala Ile Pro Arg Lys Ile Trp Leu Asp Pro Ser
 355 360 365
 Gly Lys Gln Leu Val Gln Trp Pro Val Glu Glu Leu Glu Lys Leu Arg
 370 375 380
 Gly Lys Pro Val Thr Val Gly Asp Lys Val Val Lys Pro Gly Gln His
 385 390 395 400
 Phe Glu Val Thr Gly Leu Gln Ser Tyr Gln Ser Asp Val Glu Val Ser
 405 410 415
 Phe Glu Val Ser Ser Leu Asp Lys Ala Glu Pro Phe Asp Pro Ala Tyr
 420 425 430
 Ser Asn Asp Ala Gln Lys Leu Cys Gly Ile Lys Gly Ala Asp Ala Asn
 435 440 445
 Gly Gly Val Gly Pro Phe Gly Leu Val Val Leu Ala Ser Ala Asp Leu
 450 455 460
 Ala Glu Lys Thr Ala Val Phe Phe Arg Val Phe Lys Asp Gly Tyr Gly
 465 470 475 480

Lys Pro Ile Val Leu Met Cys Ser Asp Pro Thr Lys Ser Ser Leu Thr
 485 490 495
 Pro Asp Leu Tyr Lys Pro Thr Phe Ala Gly Phe Val Asp Thr Asp Ile
 500 505 510
 Ser Ser Gly Lys Ile Ser Leu Arg Ser Leu Ile Asp Arg Ser Val Val
 515 520 525
 Glu Ser Phe Gly Ala Gly Gly Lys Thr Cys Ile Leu Ser Arg Val Tyr
 530 535 540
 Pro Ser Met Ala Leu Gly Lys Asn Ala His Leu His Val Phe Asn Asn
 545 550 555 560
 Gly Glu Thr Asp Ile Lys Val Ser Lys Leu Thr Val Trp Glu Met Lys
 565 570 575
 Arg Pro Leu Met Asn Gly Ala
 580

<210> 84

<211> 346

<212> PRT

<213> Lolium perenne

<400> 84

Met Tyr Tyr Asn Gly Ile Tyr His Glu Phe Tyr Gln Tyr Asn Pro Asn
 1 5 10 15
 Gly Ser Leu Trp Gly Asn Ile Ile Trp Gly His Ser Val Ser Thr Asp
 20 25 30
 Leu Ile Asn Trp Ile Pro Val Glu Pro Ala Ile Glu Arg Asp Ile Pro
 35 40 45
 Ser Asp Ile Asn Gly Cys Trp Thr Gly Ser Ala Thr Ile Ile Ser Gly
 50 55 60
 Asp Gln Pro Ile Ile Ile Tyr Thr Gly Ala Asp Lys Glu Asn Arg Gln
 65 70 75 80
 Leu Gln Asn Ile Val Leu Pro Lys Asn Lys Ser Asp Pro Tyr Leu Arg
 85 90 95
 Glu Trp Thr Lys Ala Gly Asn Asn Pro Val Ile Gln Pro Val Gly Pro
 100 105 110
 Gly Leu Asn Ala Ser Gln Phe Arg Asp Pro Thr Thr Gly Trp Ile Gly
 115 120 125
 Pro Asp Gly Leu Trp Arg Ile Ala Val Gly Ala Glu Leu Asn Gly Tyr
 130 135 140
 Gly Ala Ala Leu Leu Tyr Lys Ser Gln Asp Phe Leu Asn Trp Thr Arg
 145 150 155 160
 Val Asp His Pro Leu Tyr Ser Ser Asn Ala Ser Ser Met Trp Glu Cys
 165 170 175
 Pro Asp Phe Phe Ala Val Leu Pro Gly Asn Ser Gly Gly Leu Asp Leu
 180 185 190
 Ser Ala Glu Ile Pro Asn Gly Ala Lys His Val Leu Lys Met Ser Leu
 195 200 205
 Asp Ser Cys Asp Lys Tyr Met Ile Gly Val Tyr Asp Leu Lys Ser Asp
 210 215 220
 Thr Phe Met Pro Asp Ser Val Leu Asp Asp Arg Arg Leu Trp Ser Arg
 225 230 235 240
 Ile Asp His Gly Asn Phe Tyr Ala Ser Lys Ser Phe Phe Asp Ser Lys
 245 250 255
 Lys Gly Arg Arg Ile Ile Trp Gly Trp Thr Asn Glu Thr Asp Ser Ser
 260 265 270
 Ser Asp Asp Val Ala Lys Gly Trp Ala Gly Ile His Ala Ile Pro Arg
 275 280 285
 Thr Ile Trp Leu Asp Ser Tyr Gly Lys Gln Leu Leu Gln Trp Pro Ile
 290 295 300
 Glu Glu Ile Glu Ser Leu Arg Arg Asn Glu Ile Ser His Gln Gly Leu
 305 310 315 320
 Glu Leu Lys Lys Gly Asp Leu Phe Glu Ile Lys Gly Thr Asp Thr Ser
 325 330 335
 Gln Val Val His Val Phe Leu Gly Lys Leu
 340 345

<210> 85
 <211> 581
 <212> PRT
 <213> Festuca arundinacea

<400> 85
 Met Ala Gly Leu Arg Leu Ala Ala Val Ala Phe His Leu Cys Leu Leu
 1 5 10 15
 Leu Ser Pro Ser Ser Ser Leu Arg Arg Leu Tyr His Glu Asp Asp Glu
 20 25 30
 Ala Glu Ser Thr Pro Gly His Gly Gly Ser Arg Thr Ala Tyr His Phe
 35 40 45
 Gln Pro Ala Lys Asn Trp Gln Asn Asp Pro Asn Gly Pro Met Tyr His
 50 55 60
 Asn Gly Leu Tyr His Leu Phe Tyr Gln Tyr Asn Pro Arg Gly Ala Thr
 65 70 75 80
 Trp Gly Asn Gly Asn Leu Ser Trp Gly His Ser Val Ser Val Asp Leu
 85 90 95
 Val Asn Trp Ala Ala Leu Asp Thr Ala Leu Asp Pro Asp Ser Pro Phe
 100 105 110
 Asp Ala Asn Gly Cys Trp Ser Gly Ser Ala Thr Ile Leu Pro Asp Gly
 115 120 125
 Gln Pro Ala Ile Leu Tyr Thr Gly Ile Asp Ala Ala Gly Asn Gln Val
 130 135 140
 Gln Asn Val Ala Phe Pro Lys Lys Ala Ser Asp Pro Leu Leu Arg Glu
 145 150 155 160
 Trp Val Lys Pro Asp Tyr Asn Pro Val Ile Pro Leu Pro Lys Asp Val
 165 170 175
 Val His Asp Ser Phe Arg Asp Pro Ser Thr Ala Trp Arg Gly Arg Asp
 180 185 190
 Gly Leu Trp Arg Val Ala Ile Ala Ala Lys Val Asn Val Thr Val Thr
 195 200 205
 Val Gly Ser Thr Leu Ile Tyr Arg Ser Lys Asp Phe Arg Arg Trp Glu
 210 215 220
 Arg Asn Ala Ala Pro Leu Tyr Glu Ser Leu Ala Ala Gly Met Val Glu
 225 230 235 240
 Cys Pro Asp Leu Phe Pro Val Ala Lys Pro Gly Ala Gln Asn Gly Leu
 245 250 255
 Asp Tyr Ala Pro Ser Ser Arg Ala Ala Arg His Val Leu Lys Leu Ser
 260 265 270
 Val Val Ala Thr Leu Gln Asp Tyr Tyr Val Val Gly Leu Tyr Asp Asp
 275 280 285
 Thr Ala Asp Thr Phe Asn Ala Ala Ala Gly Ala Asp Asn Asp Trp Arg
 290 295 300
 Thr Trp Arg Arg Ile Asp Tyr Gly His Val Tyr Ala Ser Lys Ser Phe
 305 310 315 320
 Phe Asp Ala Arg Lys Asn Arg Arg Val Leu Trp Cys Trp Ala Asn Glu
 325 330 335
 Ser Asp Thr Glu Ala Asp Tyr Ile Ala Arg Gly Trp Ser Gly Val Gln
 340 345 350
 Thr Val Pro Arg Lys Ile Trp Leu Asp Ile Asp Gly Lys Gln Leu Leu
 355 360 365
 Gln Trp Pro Ile Lys Glu Ile Glu Thr Leu Arg Lys Lys Arg Val Gly
 370 375 380
 Leu Leu Gly Thr Glu Met Asn Ser Gly Gly Leu Asn Glu Ile Ile Gly
 385 390 395 400
 Val Ala Gly Ser Gln Ala Asp Val Glu Val Val Phe Lys Ile Pro Thr
 405 410 415
 Leu Glu Gly Ala Glu Asn Ile Glu Pro Asn Glu Leu Leu Asp Pro Gln
 420 425 430
 Lys Leu Cys Gly Asn Asn Gly Ala Ser Met Arg Gly Ser Ile Gly Pro
 435 440 445
 Phe Gly Leu Leu Leu Leu Ala Ser Gly Asp Leu Leu Glu His Thr Ser
 450 455 460
 Val Phe Phe Arg Val Phe Lys His Gly Ala Lys Tyr Lys Val Leu Met
 465 470 475 480

[illegible]

Ala Gly Ile Gln Ala Ile Pro Arg Lys Val Trp Leu Asp Pro Ser Gly
 355 360 365
 Arg Gln Leu Met Gln Trp Pro Val Glu Glu Val Lys Ala Leu Arg Gly
 370 375 380
 Lys Lys Pro Val Ser Leu Lys Asp Arg Met Val Lys Arg Gly Glu His
 385 390 395 400
 Val Glu Val Thr Gly Leu Gln Thr Ala Gln Ala Asp Val Glu Val Ser
 405 410 415
 Phe Glu Val Pro Ser Leu Glu Gly Ala Glu Ala Leu Asp Pro Ala Leu
 420 425 430
 Ala Asn Asp Ala Gln Lys Leu Cys Gly Val Lys Gly Ala Asp Val Glu
 435 440 445
 Gly Gly Val Gly Pro Phe Gly Leu Trp Val Leu Ala Ser Ser Lys Leu
 450 455 460
 Glu Glu Arg Thr Ala Val Phe Phe Arg Val Phe Lys Ala Ala Gly Asn
 465 470 475 480
 Val Asn Ser Thr Lys Pro Leu Val Leu Met Cys Ser Asp Pro Thr Lys
 485 490 495
 Ser Ser Leu Asn Lys Asn Leu Tyr His Pro Thr Phe Ala Gly Phe Val
 500 505 510
 Asp Ile Asp Met Ala Lys Gly Lys Ile Ser Leu Arg Ser Leu Ile Asp
 515 520 525
 Gln Ser Val Val Glu Ser Phe Gly Ala Gly Gly Arg Thr Cys Ile Leu
 530 535 540
 Ser Arg Val Tyr Pro Ser Leu Ala Ile Gly Arg Asn Ala His Leu His
 545 550 555 560
 Val Phe Asn Asn Gly Lys Ala Asp Ile Lys Val Ser Arg Leu Thr Ala
 565 570 575
 Trp Glu Met Lys Lys Pro Ala Leu Met Asn Gly Ala
 580 585

<210> 87

<211> 668

<212> PRT

<213> Lolium perenne

<400> 87

Met Glu Ala Arg Asp Gly Val Ser Met Pro Tyr Ser Tyr Ala Ala Leu
 1 5 10 15
 Pro Glu Asp Ala Glu Ala Ala Val Val Gly Arg Gly Arg Arg Thr Gly
 20 25 30
 Pro Leu Phe Ala Ala Leu Leu Leu Thr Leu Val Ala Ala Leu Ala
 35 40 45
 Val Ala Ala Leu Ala Gly Val Arg Leu Val Gly Glu Leu Pro Ala Gly
 50 55 60
 Gly Val Val Met Pro Asn His Pro Met Glu Val Met Asp Val Ser Gly
 65 70 75 80
 Ser Arg Gly Pro Glu Ser Gly Val Ser Glu Lys Thr Ser Gly Ala Ala
 85 90 95
 Ser Glu Ser Gly Gly Met Leu Gly Ala Asp Ala Gly Ser Asn Ala Phe
 100 105 110
 Pro Trp Ser Asn Ala Met Leu Gln Trp Gln Arg Thr Gly Phe His Phe
 115 120 125
 Gln Pro Glu Lys Asn Trp Met Asn Asp Pro Asn Gly Pro Val Tyr Tyr
 130 135 140
 Lys Gly Trp Tyr His Leu Phe Tyr Gln Tyr Asn Pro Glu Gly Ala Ile
 145 150 155 160
 Trp Gly Asn Lys Ile Ala Trp Gly His Ala Val Ser Arg Asp Met Leu
 165 170 175
 Arg Trp Arg His Leu Pro Ile Ala Met Phe Pro Asp Gln Trp Tyr Asp
 180 185 190
 Ile Asn Gly Ala Trp Ser Gly Ser Ala Thr Val Leu Pro Asp Gly Arg
 195 200 205
 Ile Val Met Leu Tyr Thr Gly Ser Thr Asn Ala Ser Val Gln Val Gln
 210 215 220

Cys Leu Ala Phe Pro Ser Asp Pro Ser Asp Pro Leu Leu Thr Asn Trp
 225 230 235 240
 Thr Lys Tyr Glu Gly Asn Pro Val Leu Tyr Pro Pro Pro His Val Gly
 245 250 255
 Glu Lys Asp Phe Arg Asp Pro Thr Thr Ala Trp Tyr Asp Gly Ser Asp
 260 265 270
 Gly Met Trp Arg Ile Val Ile Gly Ser Lys Asp Asn Arg Arg Ala Gly
 275 280 285
 Met Ala Leu Thr Tyr Lys Thr Lys Asn Phe His Asp Phe Glu Leu Val
 290 295 300
 Pro Gly Val Leu His Arg Val Pro Ala Thr Gly Met Trp Glu Cys Ile
 305 310 315 320
 Asp Leu Tyr Pro Val Gly Gly Ala Arg Gly Ile Asp Met Thr Glu Ala
 325 330 335
 Val Ala Ala Ala Ser Asn Ser Gly Gly Gly Glu Val Leu His Val Met
 340 345 350
 Lys Glu Ser Ser Asp Asp Asp Arg His Asp Tyr Tyr Ala Leu Gly Arg
 355 360 365
 Tyr Asp Ala Ala Thr Asn Lys Trp Thr Pro Leu Asp Ala Asp Ala Asp
 370 375 380
 Val Gly Ile Gly Leu Arg Tyr Asp Trp Gly Lys Phe Tyr Ala Ser Lys
 385 390 395 400
 Thr Phe Tyr Asp Pro Ala Lys Lys Arg Arg Val Leu Trp Gly Trp Val
 405 410 415
 Gly Glu Thr Asp Ser Glu Arg Ala Asp Val Ala Lys Gly Trp Ala Ser
 420 425 430
 Leu Gln Ser Ile Pro Arg Thr Val Val Leu Asp Thr Lys Thr Gly Ser
 435 440 445
 Asn Leu Ile Gln Trp Pro Val Val Glu Val Glu Thr Leu Arg Thr Asn
 450 455 460
 Ser Thr Asn Leu Gly Ser Ile Ile Val Glu His Gly Ser Val Phe Pro
 465 470 475 480
 Leu Ser Leu His Arg Ala Thr Gln Leu Asp Ile Glu Ala Ser Phe Arg
 485 490 495
 Leu Asp Pro Leu Asp Val Ala Ala Ala Lys Glu Ala Asp Val Gly Tyr
 500 505 510
 Asn Cys Ser Thr Ser Gly Gly Ala Ala Gly Arg Gly Ala Leu Gly Pro
 515 520 525
 Phe Gly Leu Leu Val Leu Ala Asp Ala Arg Arg His Gly Gly Asp Thr
 530 535 540
 Glu Gln Thr Ala Val Tyr Phe Tyr Val Ala Arg Gly Leu Asp Gly Asn
 545 550 555 560
 Leu Arg Thr His Phe Cys His Asp Glu Ser Arg Ser Ser Arg Ala Asn
 565 570 575
 Asp Ile Val Lys Arg Val Val Gly Asn Ile Val Pro Val Leu Asp Gly
 580 585 590
 Lys Ala Leu Ser Val Arg Val Leu Val Ala His Ser Ile Val Glu Ser
 595 600 605
 Phe Ala Gln Gly Gly Arg Ser Val Val Thr Ser Arg Val Tyr Pro Thr
 610 615 620
 Glu Ala Ile Tyr Ala Asn Ala Gly Val Tyr Leu Phe Asn Asn Ala Thr
 625 630 635 640
 Gly Ala Arg Val Pro Ala Thr Ser Leu Val Val His Lys Met Asp Pro
 645 650 655
 Ser Tyr Asn Gln Asn Gln Ala Glu Met Ala Ser Leu
 660 665

<210> 88

<211> 473

<212> PRT

<213> Lolium perenne

<400> 88

Val His Trp Arg His Leu Pro Leu Ala Met Val Pro Asp Gln Trp Tyr
 1 5 10 15

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Asp Ile Asn Gly Val Trp Thr Gly Ser Ala Thr Val Phe Pro Asp Gly
      20      25      30
Thr Leu Asn Met Leu Tyr Thr Gly Ser Thr Asn Ala Ser Val Gln Ala
      35      40      45
Gln Cys Leu Ala Val Pro Glu Asp Pro Asn Asp Ser Leu Leu Arg Asn
      50      55      60
Trp Thr Lys His Glu Ala Asn Pro Val Leu Leu Pro Pro Pro Gly Ile
      65      70      75      80
Gly Asp Lys Asp Phe Arg Asp Pro Thr Thr Ala Trp Phe Asp Glu Ser
      85      90      95
Asp Gln Thr Trp Arg Thr Val Ile Gly Ser Lys Asp Asn Asn Gly His
      100      105      110
Ala Gly Ile Ala Met Val Tyr Lys Thr Lys Asp Phe Leu Asn Tyr Glu
      115      120      125
Leu Ile Pro Gly Tyr Leu His Arg Val Asp Gly Thr Gly Met Trp Glu
      130      135      140
Cys Ile Asp Phe Tyr Pro Val Gly Gly Lys Asn Gly Ser Glu Glu Leu
      145      150      155      160
Tyr Val Ile Lys Glu Ser Ser Asp Asp Asp Arg His Asp Trp Tyr Thr
      165      170      175
Leu Gly Lys Tyr Asp Ala Ala Ala Asn Thr Phe Thr Ala Ala Asp Pro
      180      185      190
Glu Asn Asp Leu Gly Ile Gly Leu Arg Tyr Asp Trp Gly Lys Phe Tyr
      195      200      205
Ala Ser Lys Thr Phe Tyr Asp Pro Ala Lys Lys Arg Arg Val Leu Trp
      210      215      220
Gly Trp Ile Gly Glu Thr Asp Ser Glu Arg Ala Asp Val Ala Lys Gly
      225      230      235      240
Trp Ala Ser Leu Met Ser Ile Pro Arg Thr Val Glu Leu Asp Glu Lys
      245      250      255
Thr Trp Thr Asn Leu Ile Gln Trp Pro Val Glu Glu Ile Glu Thr Leu
      260      265      270
Arg Ile Lys Ser Thr Asp Leu Gly Gly Ile Thr Ile Asp His Gly Ser
      275      280      285
Val Tyr Pro Leu Pro Leu His Arg Ala Thr Gln Leu Asp Ile Glu Ala
      290      295      300
Ser Phe Arg Leu Asp Ala Ala Thr Val Ala Ala Leu Asn Glu Ala Asp
      305      310      315      320
Val Gly Tyr Asn Cys Ser Thr Ser Gly Gly Ser Thr His Arg Gly Ala
      325      330      335
Leu Gly Pro Phe Gly Ile Leu Val Leu Ala Asp Gly Lys Ala Glu Gln
      340      345      350
Thr Ala Val Tyr Phe Tyr Val Ser Lys Gly Leu Asp Gly Ala Leu Glu
      355      360      365
Thr His Phe Cys His Asp Glu Ser Arg Ser Thr Leu Ala Lys Asp Val
      370      375      380
Val Lys Arg Val Val Gly Tyr Thr Val Pro Val Leu Asp Gly Glu Ala
      385      390      395      400
Phe Ser Val Arg Val Leu Val Asp His Ser Ile Val Glu Ser Phe Ala
      405      410      415
Met Gly Gly Arg Ser Thr Ala Thr Ser Arg Val Tyr Pro Thr Glu Ser
      420      425      430
Ile Tyr Gly Ala Ala Gly Ala Tyr Leu Phe Asn Asn Ala Thr Gly Gly
      435      440      445
Ser Val Thr Val Glu Lys Leu Val Val His Glu Met Asp Ser Ser Tyr
      450      455      460
Asn Gln Ile Phe Met Ala Asp Asp Leu
      465      470

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<210> 89

<211> 539

<212> PRT

<213> Lolium perenne

<400> 89

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Ile Phe Arg Ser Arg Leu Pro Asp Ile Asp Ile Pro Thr His Met Pro
1      5      10      15
Leu His Asp Tyr Cys Phe Ala Thr Ala Ala Ser Ala Pro Asp Ala Pro
20     25     30
Cys Leu Ile Thr Ala Ala Thr Gly Arg Thr Tyr Thr Phe Ala Glu Thr
35     40     45
His Leu Leu Cys Arg Lys Ala Ala Ala Leu His Gly Leu Gly Val
50     55     60
Arg His Gly Asp Arg Ile Met Val Leu Leu Gln Asn Ser Val Glu Phe
65     70     75     80
Ala Leu Ala Phe Phe Gly Ala Ser Met Leu Gly Ala Val Ser Thr Ala
85     90     95
Ala Asn Pro Phe Cys Thr Pro Gln Glu Ile His Lys Gln Leu Val Ala
100    105    110
Ser Gly Ala Lys Leu Val Val Thr Gln Ser Ala Tyr Val Asp Lys Leu
115    120    125
Arg His Glu Ala Phe Pro Arg Ile Gly Glu Ala Leu Thr Val Ile Thr
130    135    140
Ile Asp Asp Asp Gly Thr Pro Asp Gly Cys Gln Pro Phe Trp Gly Leu
145    150    155    160
Val Ser Ala Ala Asp Glu Asn Ser Val Pro Glu Ser Pro Ile Ser Pro
165    170    175
Asp Asp Ala Val Ala Leu Pro Tyr Ser Ser Gly Thr Thr Gly Leu Pro
180    185    190
Lys Gly Val Val Leu Thr His Gly Gly Leu Val Ser Ser Val Ala Gln
195    200    205
Gln Val Asp Gly Glu Asn Pro Asn Leu His Met Arg Ala Gly Glu Asp
210    215    220
Val Val Leu Cys Val Leu Pro Leu Phe His Ile Phe Ser Leu Asn Ser
225    230    235    240
Val Leu Leu Cys Ala Leu Arg Ala Gly Ala Ala Val Met Leu Met Pro
245    250    255
Arg Phe Glu Met Gly Ala Met Leu Glu Gly Ile Glu Arg Trp Arg Val
260    265    270
Thr Val Ala Val Val Pro Pro Leu Val Leu Ala Leu Ala Lys Asn
275    280    285
Pro Gly Val Glu Lys His Asp Leu Ser Ser Ile Arg Ile Val Leu Ser
290    295    300
Gly Ala Ala Pro Leu Gly Lys Glu Leu Glu Asp Ala Leu Arg Gly Arg
305    310    315    320
Leu Pro Gln Ala Ile Phe Gly Gln Gly Tyr Gly Met Thr Glu Ala Gly
325    330    335
Pro Val Leu Ser Met Cys Pro Ala Phe Ala Arg Glu Pro Thr Pro Ala
340    345    350
Lys Ser Gly Ser Cys Gly Thr Val Val Arg Asn Ala Glu Leu Lys Val
355    360    365
Val Asp Pro Asp Thr Gly Val Ser Leu Gly Arg Asn Leu Pro Gly Glu
370    375    380
Ile Cys Ile Arg Gly Pro Gln Ile Met Lys Gly Tyr Leu Asn Asp Pro
385    390    395    400
Val Ala Thr Ala Ala Thr Ile Asp Val Glu Gly Trp Leu His Thr Gly
405    410    415
Asp Ile Gly Tyr Val Asp Asp Asp Asp Glu Val Phe Ile Val Asp Arg
420    425    430
Val Lys Glu Leu Ile Lys Phe Lys Gly Phe Gln Val Pro Pro Ala Glu
435    440    445
Leu Glu Ala Leu Leu Ile Ala His Pro Ser Ile Ala Asp Ala Ala Val
450    455    460
Val Pro Gln Lys Asp Asp Ala Ala Gly Glu Val Pro Val Ala Phe Val
465    470    475    480
Val Arg Ala Ala Asp Ser Asp Ile Ala Glu Glu Ala Ile Lys Glu Phe
485    490    495
Val Ser Lys Gln Val Val Phe Tyr Lys Arg Leu His Lys Val Tyr Phe
500    505    510

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Thr His Ala Ile Pro Lys Ser Ala Ser Gly Lys Ile Leu Arg Lys Glu
 515 520 525
 Leu Arg Ala Lys Leu Ala Ala Pro Ala Thr Ala
 530 535

<210> 90
 <211> 559
 <212> PRT
 <213> Lolium perenne

<400> 90
 Met Gly Ser Ile Ala Ala Asp Leu Ala Pro Glu Ala Pro Ala Glu Leu
 1 5 10 15
 Val Phe Arg Ser Lys Leu Pro Asp Ile Glu Ile Pro Thr His Leu Thr
 20 25 30
 Leu Gln Asp Tyr Cys Phe Glu Arg Leu Pro Glu Leu Ser Ala Arg Ala
 35 40 45
 Cys Leu Ile Asp Gly Ala Thr Gly Ala Ala Leu Thr Tyr Gly Glu Val
 50 55 60
 Asp Ala Leu Ser Arg Arg Cys Ala Ala Gly Leu Arg Arg Leu Gly Val
 65 70 75 80
 Arg Lys Gly Asp Val Val Met Ala Leu Leu Arg Asn Cys Pro Glu Phe
 85 90 95
 Ala Phe Val Phe Leu Gly Ala Ala Arg Leu Gly Ala Ala Thr Thr Thr
 100 105 110
 Ala Asn Pro Phe Tyr Thr Pro His Glu Ile His Arg Gln Ala Ala Ala
 115 120 125
 Ala Gly Ala Lys Val Ile Val Thr Glu Ala Cys Ala Val Glu Lys Val
 130 135 140
 Arg Ala Phe Ala Ala Glu Arg Gly Ile Pro Val Val Ser Val Asp Glu
 145 150 155 160
 Ala Val Asp Asp Gly Cys Leu Pro Phe Ala Ala Thr Leu Leu Gly Glu
 165 170 175
 Glu Ser Gly Glu Arg Phe Val Asp Glu Ala Val Asp Pro Asp Asp Val
 180 185 190
 Val Ala Leu Pro Tyr Ser Ser Gly Thr Thr Gly Leu Pro Lys Gly Val
 195 200 205
 Met Leu Thr His Arg Ser Leu Val Thr Ser Val Ala Gln Gln Val Asp
 210 215 220
 Gly Glu Asn Pro Asn Leu His Phe Ser Ser Ser Asp Val Leu Leu Cys
 225 230 235 240
 Val Leu Pro Leu Phe His Ile Tyr Ser Leu Asn Ser Val Leu Leu Ala
 245 250 255
 Gly Leu Arg Ala Gly Cys Ala Ile Val Ile Met Arg Lys Phe Asp His
 260 265 270
 Gly Ala Leu Val Asp Leu Val Arg Ala His Gly Val Thr Val Ala Pro
 275 280 285
 Phe Val Pro Pro Ile Val Val Glu Ile Ala Lys Ser Ala Arg Val Thr
 290 295 300
 Ala Ala Asp Leu Ala Ser Ile Arg Leu Val Met Ser Gly Ala Ala Pro
 305 310 315 320
 Met Gly Lys Glu Leu Gln Asp Ala Phe Met Ala Lys Ile Pro Asn Ala
 325 330 335
 Val Leu Gly Gln Gly Tyr Gly Met Thr Glu Ala Gly Pro Val Leu Ala
 340 345 350
 Met Cys Leu Ala Phe Ala Lys Glu Pro Phe Glu Val Lys Ser Gly Ser
 355 360 365
 Cys Gly Thr Val Val Arg Asn Ala Glu Leu Lys Ile Val Asp Pro Asp
 370 375 380
 Thr Gly Ala Ser Leu Gly Arg Asn Leu Pro Gly Glu Ile Cys Ile Arg
 385 390 395 400
 Gly Lys Gln Ile Met Lys Gly Tyr Leu Asn Asp Pro Glu Ala Thr Lys
 405 410 415
 Asn Thr Ile Asp Lys Asp Gly Trp Leu His Thr Gly Asp Ile Gly Tyr
 420 425 430

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Val Asp Asp Asp Asp Glu Ile Phe Ile Val Asp Arg Leu Lys Glu Ile
      435      440      445
Ile Lys Tyr Lys Gly Phe Gln Val Pro Pro Ala Glu Leu Glu Ala Leu
      450      455      460
Leu Ile Thr His Pro Glu Ile Lys Asp Ala Ala Val Val Ser Met Gln
      465      470      475      480
Asp Glu Leu Ala Gly Glu Val Pro Val Ala Phe Val Val Arg Thr Glu
      485      490      495
Gly Ser Glu Ile Ser Glu Asn Glu Ile Lys Gln Phe Val Ala Lys Glu
      500      505      510
Val Val Phe Tyr Lys Arg Ile Cys Lys Val Phe Phe Ala Asp Ser Ile
      515      520      525
Pro Lys Ser Pro Ser Gly Lys Ile Leu Arg Lys Asp Leu Arg Ala Lys
      530      535      540
Leu Ala Ala Gly Ile Pro Gly Ser Asp Thr Thr Gln Ser Lys Asn
      545      550      555

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<210> 91

<211> 559

<212> PRT

<213> Festuca arundinacea

<400> 91

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Met Gly Ser Ile Ala Ala Asp Ala Pro Glu Ala Pro Pro Ala Glu Leu
  1      5      10      15
Val Phe Arg Ser Lys Leu Pro Asp Ile Glu Ile Pro Thr His Leu Thr
      20      25      30
Leu Gln Asp Tyr Cys Phe Gln Arg Leu Pro Glu His Ser Ala Arg Ala
      35      40      45
Cys Leu Ile Asp Gly Ala Thr Gly Ala Ala Leu Thr Tyr Gly Glu Val
      50      55      60
Asp Ala Leu Ser Arg Arg Cys Ala Ala Gly Leu Arg Arg Leu Gly Val
      65      70      75      80
Arg Lys Gly Asp Val Val Met Ala Leu Leu Arg Asn Cys Pro Glu Phe
      85      90      95
Ala Phe Val Phe Leu Gly Ala Ala Arg Leu Gly Ala Ala Thr Thr Thr
      100      105      110
Ala Asn Pro Phe Tyr Thr Pro His Glu Ile His Arg Gln Ala Thr Ala
      115      120      125
Ala Gly Ala Lys Val Ile Val Thr Glu Ala Cys Ala Val Glu Lys Val
      130      135      140
Arg Ala Phe Ala Ala Glu Arg Gly Ile Thr Val Val Ser Val Asp Glu
      145      150      155      160
Gly Val Asp Asp Gly Cys Leu Pro Phe Gly Glu Thr Leu Leu Gly Glu
      165      170      175
Asp Gly Gly Glu Arg Phe Val Asp Glu Ala Val Asp Pro Asp Asp Val
      180      185      190
Val Ala Leu Pro Tyr Ser Ser Gly Thr Thr Gly Leu Pro Lys Gly Val
      195      200      205
Met Leu Thr His Arg Ser Leu Val Thr Ser Val Ala Gln Gln Val Asp
      210      215      220
Gly Glu Asn Pro Asn Leu His Phe Ser Ser Ser Asp Val Leu Leu Cys
      225      230      235      240
Val Leu Pro Leu Phe His Ile Tyr Ser Leu Asn Ser Val Leu Leu Ala
      245      250      255
Gly Leu Arg Ala Gly Cys Ala Ile Val Ile Met Arg Lys Phe Asp His
      260      265      270
Gly Ala Leu Val Asp Leu Val Arg Ala His Gly Val Thr Val Ala Pro
      275      280      285
Phe Val Pro Pro Ile Val Val Glu Ile Ala Lys Ser Ala Arg Val Thr
      290      295      300
Ala Ala Asp Leu Ala Ser Ile Arg Leu Val Met Ser Gly Ala Ala Pro
      305      310      315      320
Met Gly Lys Glu Leu Gln Asp Ala Phe Met Ala Lys Ile Pro Asn Ala
      325      330      335

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Val Leu Gly Gln Gly Tyr Gly Met Thr Glu Ala Gly Pro Val Leu Ala
 340 345 350
 Met Cys Leu Ala Phe Ala Lys Glu Pro Phe Glu Val Lys Ser Gly Ser
 355 360 365
 Cys Gly Thr Val Val Arg Asn Ala Glu Leu Lys Ile Val Asp Pro Asp
 370 375 380
 Thr Gly Ala Ser Leu Gly Arg Asn Leu Pro Gly Glu Ile Cys Ile Arg
 385 390 395 400
 Gly Lys Gln Ile Met Lys Gly Tyr Leu Asn Asp Pro Glu Ala Thr Lys
 405 410 415
 Asn Thr Ile Asp Lys Asp Gly Trp Leu His Thr Gly Asp Ile Gly Tyr
 420 425 430
 Val Asp Asp Asp Glu Ile Phe Ile Val Asp Arg Leu Lys Glu Ile
 435 440 445
 Ile Lys Tyr Lys Gly Phe Gln Val Pro Pro Ala Glu Leu Glu Ala Leu
 450 455 460
 Leu Ile Thr His Pro Glu Ile Lys Asp Ala Ala Val Val Ser Met Gln
 465 470 475 480
 Asp Glu Leu Ala Gly Glu Val Pro Val Ala Phe Val Val Arg Thr Glu
 485 490 495
 Gly Ser Glu Ile Ser Glu Asn Glu Ile Lys Gln Phe Val Ala Lys Glu
 500 505 510
 Val Val Phe Tyr Lys Arg Ile Cys Lys Val Phe Phe Ala Asp Ser Ile
 515 520 525
 Pro Lys Ser Pro Ser Gly Lys Ile Leu Arg Lys Asp Leu Arg Ala Lys
 530 535 540
 Leu Ala Ala Gly Ile Pro Gly Ser Glu Thr Thr Gln Ser Lys Ser
 545 550 555

<210> 92

<211> 557

<212> PRT

<213> Lolium perenne

<400> 92

Met Gly Ser Val Pro Glu Glu Ser Val Val Ser Val Ala Ala Ala Glu
 1 5 10 15
 Thr Val Phe Arg Ser Lys Leu Pro Asp Ile Glu Ile Asn Asn Glu Gln
 20 25 30
 Thr Leu Gln Ser Tyr Cys Phe Glu Lys Met Ala Glu Val Ala Ser Arg
 35 40 45
 Pro Cys Ile Ile Asp Gly Gln Thr Gly Ala Ser Tyr Thr Thr Glu
 50 55 60
 Val Asp Tyr Leu Thr Arg Arg Ala Ala Ala Gly Leu Arg Arg Met Gly
 65 70 75 80
 Val Gly Lys Gly Asp Val Val Met Asn Leu Leu Arg Asn Cys Pro Glu
 85 90 95
 Phe Ala Phe Ser Phe Leu Gly Ala Ala Arg Leu Gly Ala Ala Thr Thr
 100 105 110
 Thr Ala Asn Pro Phe Tyr Thr Pro His Glu Ile His Arg Gln Ala Glu
 115 120 125
 Ala Ala Gly Ala Lys Leu Ile Val Thr Glu Ala Cys Ala Val Glu Lys
 130 135 140
 Val Leu Glu Phe Ala Ala Gly Arg Gly Leu Pro Val Val Thr Val Asp
 145 150 155 160
 Gly Arg Arg Asp Gly Cys Val Asp Phe Ala Glu Leu Ile Ala Gly Glu
 165 170 175
 Glu Leu Pro Glu Ala Asp Glu Ala Gly Ile Leu Pro Asp Asp Val Val
 180 185 190
 Ala Leu Pro Tyr Ser Ser Gly Thr Thr Gly Leu Pro Lys Gly Val Met
 195 200 205
 Leu Thr His Arg Ser Leu Val Thr Ser Val Ala Gln Leu Val Asp Gly
 210 215 220
 Ser Asn Pro Asn Val Cys Phe Asn Lys Asp Asp Ala Leu Leu Cys Leu
 225 230 235 240

Leu Pro Leu Phe His Ile Tyr Ser Leu His Thr Val Leu Leu Ala Gly
 245 250 255
 Leu Arg Val Gly Ala Ala Ile Val Ile Met Arg Lys Phe Asp Val Gly
 260 265 270
 Ala Leu Val Asp Leu Val Arg Ala His Arg Ile Thr Ile Ala Pro Phe
 275 280 285
 Val Pro Pro Ile Val Val Glu Ile Ala Lys Ser Asp Arg Val Gly Ala
 290 295 300
 Asp Asp Leu Ala Ser Ile Arg Met Val Leu Ser Gly Ala Ala Pro Met
 305 310 315 320
 Gly Lys Asp Leu Gln Asp Ala Phe Met Ala Lys Ile Pro Asn Ala Val
 325 330 335
 Leu Gly Gln Gly Tyr Gly Met Thr Glu Ala Gly Pro Val Leu Ala Met
 340 345 350
 Cys Leu Ala Phe Ala Lys Glu Pro Phe Lys Val Lys Ser Gly Ser Cys
 355 360 365
 Gly Thr Val Val Arg Asn Ala Glu Leu Lys Val Val Asp Pro Asp Thr
 370 375 380
 Gly Ala Ser Leu Gly Arg Asn Gln Pro Gly Glu Ile Cys Val Arg Gly
 385 390 395 400
 Lys Gln Ile Met Ile Gly Tyr Leu Asn Asp Pro Glu Ser Thr Lys Asn
 405 410 415
 Thr Ile Asp Lys Asp Gly Trp Leu His Thr Gly Asp Ile Gly Leu Val
 420 425 430
 Asp Asp Asp Asp Glu Ile Phe Ile Val Asp Arg Leu Lys Glu Ile Ile
 435 440 445
 Lys Tyr Lys Gly Phe Gln Val Ala Pro Ala Glu Leu Glu Ala Leu Leu
 450 455 460
 Leu Thr Asn Pro Glu Val Lys Asp Ala Ala Val Val Gly Val Lys Asp
 465 470 475 480
 Asp Leu Cys Gly Glu Val Pro Val Ala Phe Ile Lys Arg Ile Glu Gly
 485 490 495
 Ser Glu Ile Thr Glu Asn Glu Ile Lys Gln Phe Val Ser Lys Glu Val
 500 505 510
 Val Phe Tyr Lys Arg Ile Asn Lys Val Tyr Phe Thr Asp Ser Ile Pro
 515 520 525
 Lys Asn Pro Ser Gly Lys Ile Val Arg Lys Asp Leu Arg Ala Arg Leu
 530 535 540
 Ala Ala Gly Ile Pro Thr Glu Val Ala Ala Pro Arg Ser
 545 550 555

<210> 93

<211> 557

<212> PRT

<213> Festuca arundinacea

<400> 93

Met Gly Ser Val Pro Glu Glu Ser Val Val Ala Ala Ala Val Ala Glu
 1 5 10 15
 Thr Val Phe Arg Ser Lys Leu Pro Asp Ile Glu Ile Asn Asn Glu Gln
 20 25 30
 Thr Leu Gln Ser Tyr Cys Phe Glu Lys Met Ala Glu Val Ala Ser Arg
 35 40 45
 Pro Cys Ile Ile Asp Gly Gln Thr Gly Ala Ser Tyr Thr Tyr Thr Glu
 50 55 60
 Val Glu Ser Leu Thr Arg Arg Ala Ala Ala Gly Leu Arg Arg Met Gly
 65 70 75 80
 Val Gly Lys Gly Asp Val Val Met Asn Leu Leu Arg Asn Cys Pro Glu
 85 90 95
 Phe Ala Phe Ser Phe Leu Gly Ala Ala Arg Leu Gly Ala Ala Thr Thr
 100 105 110
 Thr Ala Asn Pro Phe Tyr Thr Pro His Glu Ile His Arg Gln Ala Glu
 115 120 125
 Ala Ala Gly Ala Lys Val Ile Val Thr Glu Ala Cys Ala Val Glu Lys
 130 135 140

Val Leu Glu Phe Ala Ala Glu Arg Gly Leu Pro Val Val Thr Val Asp
 145 150 155 160
 Gly Lys Arg Asp Gly Cys Val Asp Phe Ala Glu Leu Ile Ala Gly Glu
 165 170 175
 Glu Leu Pro Glu Ala Glu Glu Ala Gly Ile Leu Pro Asp Asp Val Val
 180 185 190
 Ala Leu Pro Tyr Ser Ser Gly Thr Thr Gly Leu Pro Lys Gly Val Met
 195 200 205
 Leu Thr His Arg Ser Leu Val Thr Ser Val Ala Gln Leu Phe Asp Gly
 210 215 220
 Ser Asn Pro Asn Val Cys Phe Asn Lys Asp Asp Ala Leu Leu Cys Leu
 225 230 235 240
 Leu Pro Leu Phe His Ile Tyr Ser Leu His Thr Val Leu Leu Ala Gly
 245 250 255
 Leu Arg Val Gly Ala Ala Ile Val Ile Met Arg Lys Phe Asp Val Gly
 260 265 270
 Ala Leu Val Asp Leu Val Arg Ala His Arg Ile Thr Ile Ala Pro Phe
 275 280 285
 Val Pro Pro Ile Val Val Glu Ile Ala Lys Ser Asp Arg Val Thr Ala
 290 295 300
 Asp Asp Leu Thr Ser Ile Arg Met Val Leu Ser Gly Ala Ala Pro Met
 305 310 315 320
 Gly Lys Asp Leu Gln Asp Ala Phe Met Ala Lys Ile Pro Asn Ala Val
 325 330 335
 Leu Gly Gln Gly Tyr Gly Met Thr Glu Ala Gly Pro Val Leu Ala Met
 340 345 350
 Cys Leu Ala Phe Ala Lys Glu Pro Phe Lys Val Lys Ser Gly Ser Cys
 355 360 365
 Gly Thr Val Val Arg Asn Ala Glu Leu Lys Val Val Asp Pro Asp Thr
 370 375 380
 Gly Ala Ser Leu Gly Arg Asn Gln Pro Gly Glu Ile Cys Val Arg Gly
 385 390 395 400
 Lys Gln Ile Met Ile Gly Tyr Leu Asn Asp Pro Glu Ser Thr Lys Asn
 405 410 415
 Thr Ile Asp Lys Asp Gly Trp Leu His Thr Gly Asp Ile Gly Leu Val
 420 425 430
 Asp Asp Asp Asp Glu Ile Phe Ile Val Asp Arg Leu Lys Glu Ile Ile
 435 440 445
 Lys Tyr Lys Gly Phe Gln Val Ala Pro Ala Glu Leu Glu Ala Leu Leu
 450 455 460
 Leu Thr Asn Pro Glu Val Lys Asp Ala Ala Val Val Gly Val Lys Asp
 465 470 475 480
 Asp Leu Cys Gly Glu Val Pro Val Ala Phe Ile Lys Arg Ile Glu Gly
 485 490 495
 Ser Glu Ile Thr Glu Asn Asp Ile Lys Gln Phe Val Ser Lys Glu Val
 500 505 510
 Val Phe Tyr Lys Arg Ile Asn Lys Val Tyr Phe Thr Asp Ser Ile Pro
 515 520 525
 Lys Asn Pro Ser Gly Lys Ile Leu Arg Lys Asp Leu Arg Ala Arg Leu
 530 535 540
 Ala Ala Gly Ile Pro Thr Glu Val Ala Ala Pro Arg Ser
 545 550 555

<210> 94

<211> 501

<212> PRT

<213> Lolium perenne

<400> 94

Met Glu Val Leu Leu Leu Glu Lys Ala Leu Leu Gly Leu Phe Ala Ala
 1 5 10 15
 Ala Val Leu Ala Ile Ala Val Ala Lys Leu Ala Gly Lys Arg Phe Arg
 20 25 30
 Leu Pro Pro Gly Pro Ser Gly Ala Pro Ile Val Gly Asn Trp Leu Gln
 35 40 45

Val Gly Asp Asp Leu Asn His Arg Asn Leu Met Gly Ile Ala Lys Arg
 50 55 60
 Phe Gly Glu Val Phe Leu Leu Arg Met Gly Ile Arg Asn Leu Val Val
 65 70 75 80
 Val Ser Ser Pro Glu Leu Ala Lys Glu Val Leu His Thr Gln Gly Val
 85 90 95
 Glu Phe Gly Ser Arg Thr Arg Asn Val Val Phe Asp Ile Phe Thr Gly
 100 105 110
 Asn Gly Gln Asp Met Val Phe Thr Val Tyr Gly Asp His Trp Arg Lys
 115 120 125
 Met Arg Arg Ile Met Thr Val Pro Phe Phe Thr Asn Lys Val Val Ala
 130 135 140
 Gln Asn Arg Val Gly Trp Glu Glu Glu Ala Arg Leu Val Val Glu Asp
 145 150 155 160
 Val Lys Ala Asp Pro Ala Phe Ala Thr Ala Gly Thr Val Ile Arg Arg
 165 170 175
 Arg Leu Gln Leu Met Met Tyr Asn Asp Met Phe Arg Ile Met Phe Asp
 180 185 190
 Arg Arg Phe Glu Ser Val Asp Asp Pro Leu Phe Asn Lys Leu Lys Ala
 195 200 205
 Met Asn Ala Glu Arg Ser Ile Leu Ser Gln Ser Phe Asp Tyr Asn Tyr
 210 215 220
 Gly Asp Phe Ile Pro Ile Leu Arg Pro Phe Leu Arg Lys Tyr Leu Asn
 225 230 235 240
 Arg Cys Thr Asn Leu Thr Thr Lys Arg Met Lys Leu Phe Glu Asp His
 245 250 255
 Phe Val Ala Asp Arg Lys Lys Ala Leu Glu Gln Asn Gly Glu Ile Arg
 260 265 270
 Cys Ala Met Asp His Ile Leu Glu Ala Glu Arg Lys Gly Glu Ile Asn
 275 280 285
 His Asp Asn Val Leu Tyr Ile Val Glu Asn Ile Asn Val Ala Ala Ile
 290 295 300
 Glu Thr Thr Leu Trp Ser Ile Glu Trp Gly Ile Ala Glu Leu Val Asn
 305 310 315 320
 His Pro Asp Val Gln Ser Lys Leu Arg Asp Glu Met Thr Ala Val Leu
 325 330 335
 Gly Ala Asp Val Ala Val Thr Glu Pro Asp Leu Glu Arg Leu Pro Tyr
 340 345 350
 Leu Gln Ser Val Val Lys Glu Thr Leu Arg Leu Arg Met Ala Ile Pro
 355 360 365
 Leu Leu Val Pro His Met Asn Leu Ser Asp Ala Lys Leu Ala Gly Tyr
 370 375 380
 Asp Ile Pro Ala Glu Ser Lys Ile Leu Val Asn Ala Trp Phe Leu Ala
 385 390 395 400
 Asn Asp Pro Lys Arg Trp Val Arg Ala Asp Glu Phe Arg Pro Glu Arg
 405 410 415
 Phe Leu Glu Glu Glu Lys Ala Val Glu Ala His Gly Asn Asp Phe Arg
 420 425 430
 Phe Val Pro Phe Gly Val Gly Arg Arg Ser Cys Pro Gly Ile Val Leu
 435 440 445
 Ala Leu Pro Ile Ile Gly Ile Thr Leu Gly Arg Leu Val Gln Asn Phe
 450 455 460
 Gln Leu Leu Pro Pro Pro Gly Gln Asp Lys Ile Asp Thr Thr Glu Lys
 465 470 475 480
 Pro Gly Gln Phe Ser Asn Gln Ile Leu Lys His Ala Thr Val Val Cys
 485 490 495
 Lys Pro Leu Glu Ala
 500

<210> 95

<211> 505

<212> PRT

<213> Festuca arundinacea

<400> 95

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Met Asp Phe Val Phe Val Glu Lys Leu Leu Val Gly Leu Leu Ala Ser
 1          5          10          15
Val Val Val Ala Ile Val Val Ser Lys Ile Arg Gly Arg Lys Leu Arg
      20          25          30
Leu Pro Pro Gly Pro Ile Pro Val Pro Ile Phe Gly Asn Trp Leu Gln
      35          40          45
Val Gly Asp Asp Leu Asn His Arg Asn Leu Ala Ala Met Ala Arg Lys
      50          55          60
Phe Gly Glu Val Phe Leu Leu Arg Met Gly Ile Arg Asn Leu Val Val
      65          70          75          80
Val Ser Ser Pro Glu Leu Ala Lys Glu Val Leu His Thr Gln Gly Val
      85          90          95
Glu Phe Gly Ser Arg Thr Arg Asn Val Val Phe Asp Ile Phe Thr Gly
      100          105          110
Lys Gly Gln Asp Met Val Phe Thr Val Tyr Gly Asp His Trp Arg Lys
      115          120          125
Met Arg Arg Ile Met Thr Val Pro Phe Phe Thr Asn Lys Val Val Gln
      130          135          140
Gln Tyr Arg Ala Gly Trp Glu Ala Glu Ala Ala Phe Val Val Asp Asn
      145          150          155          160
Val Arg Ala Asp Pro Lys Ala Ala Thr Asp Gly Val Val Leu Arg Arg
      165          170          175
His Leu Gln Leu Met Met Tyr Asn Asn Met Tyr Arg Ile Met Phe Asp
      180          185          190
Arg Arg Phe Glu Ser Met Asp Asp Pro Leu Phe Leu Arg Leu Arg Ala
      195          200          205
Leu Asn Gly Glu Arg Ser Arg Leu Ala Gln Ser Phe Glu Tyr Asn Tyr
      210          215          220
Gly Asp Phe Ile Pro Val Leu Arg Pro Phe Leu Arg Gly Tyr Leu Gly
      225          230          235          240
Leu Cys Glu Gln Val Lys Glu Thr Arg Leu Lys Leu Phe Lys Asp Tyr
      245          250          255
Phe Leu Asp Glu Arg Lys Lys Leu Ala Ser Thr Lys Ser Met Asp Thr
      260          265          270
Asn Gly Leu Lys Cys Ala Ile Asp His Ile Leu Glu Ala Gln Glu Lys
      275          280          285
Gly Glu Ile Asn Glu Asp Asn Val Leu Tyr Ile Ile Glu Asn Ile Asn
      290          295          300
Val Ala Ala Ile Glu Thr Thr Leu Trp Ser Ile Glu Trp Gly Ile Ala
      305          310          315          320
Glu Leu Val Asn His Pro Glu Ile Gln Gln Lys Leu Arg Asp Glu Met
      325          330          335
Asp Ala Val Leu Gly Ala Gly His Gln Ile Thr Glu Pro Asp Thr His
      340          345          350
Lys Leu Pro Tyr Leu Gln Ala Val Ile Lys Glu Thr Leu Arg Leu Arg
      355          360          365
Met Ala Ile Pro Leu Leu Val Pro His Met Asn Leu His Asp Ala Lys
      370          375          380
Leu Ala Gly Tyr Asn Ile Pro Ala Glu Ser Lys Ile Leu Val Asn Ala
      385          390          395          400
Trp Phe Leu Ala Asn Asn Pro Glu Gln Trp Lys Arg Pro Asp Glu Phe
      405          410          415
Arg Pro Glu Arg Phe Leu Glu Glu Glu Lys His Val Glu Ala Ser Gly
      420          425          430
Asn Asp Phe Arg Phe Leu Pro Phe Gly Val Gly Arg Arg Ser Cys Pro
      435          440          445
Gly Ile Ile Leu Ala Leu Pro Ile Leu Gly Ile Thr Ile Gly Arg Leu
      450          455          460
Val Gln Asn Phe Glu Leu Thr Thr Pro Pro Gly Val Asp Lys Leu Asp
      465          470          475          480
Thr Thr Glu Lys Gly Gly Gln Phe Ser Leu His Ile Leu Asn His Ser
      485          490          495
Thr Ile Val Ala Lys Pro Arg Val Phe
      500          505

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<210> 96
 <211> 361
 <212> PRT
 <213> *Lolium perenne*

<400> 96
 Met Gly Ile Val Asn Ala Ser Glu Lys Thr Ile Thr Gly Trp Ala Ala
 1 5 10 15
 Arg Asp Ala Thr Gly His Leu Ser Pro Tyr Thr Tyr Asn Leu Arg Arg
 20 25 30
 Thr Gly Ala Glu Asp Val Val Leu Lys Val Leu Tyr Cys Gly Ile Cys
 35 40 45
 His Thr Asp Leu His Gln Thr Lys Asn His Leu Gly Ala Pro Lys Tyr
 50 55 60
 Pro Met Val Pro Gly His Glu Val Val Gly Glu Val Val Glu Val Gly
 65 70 75 80
 Pro Glu Val Ser Lys Tyr Ser Val Gly Asp Val Val Gly Val Gly Val
 85 90 95
 Ile Val Gly Cys Cys Arg Asp Cys Arg Pro Cys Lys Ala Asn Val Glu
 100 105 110
 Gln Tyr Cys Asn Lys Lys Ile Trp Ser Tyr Asn Asp Val Tyr Thr Asp
 115 120 125
 Gly Lys Pro Thr Gln Gly Gly Phe Ala Ser Ser Met Val Val Asp Gln
 130 135 140
 Lys Phe Val Val Lys Ile Pro Ala Gly Leu Ala Pro Glu Gln Ala Ala
 145 150 155 160
 Pro Leu Leu Cys Ala Gly Val Thr Val Tyr Ser Pro Leu Lys His Phe
 165 170 175
 Gly Leu Met Thr Pro Gly Leu Arg Gly Gly Ile Leu Gly Leu Gly Gly
 180 185 190
 Val Gly His Met Gly Val Lys Val Ala Lys Ser Met Gly His His Val
 195 200 205
 Thr Val Ile Ser Ser Ser Asp Lys Lys Arg Ala Glu Ala Met Asp Asp
 210 215 220
 Leu Gly Ala Asp Ala Tyr Leu Val Ser Ser Asp Glu Ala Gln Met Ala
 225 230 235 240
 Ala Ala Met Asp Ser Leu Asp Tyr Ile Ile Asp Thr Val Pro Val Lys
 245 250 255
 His Pro Leu Glu Pro Tyr Leu Ala Leu Leu Lys Met Asp Gly Lys Leu
 260 265 270
 Val Leu Met Gly Val Ile Gly Glu Pro Leu Ser Phe Val Ser Pro Met
 275 280 285
 Val Met Leu Gly Arg Lys Thr Ile Thr Gly Ser Phe Ile Gly Ser Ile
 290 295 300
 Glu Glu Thr Glu Glu Val Leu Arg Phe Cys Val Asp Lys Gly Leu Thr
 305 310 315 320
 Ser Gln Ile Glu Val Val Lys Met Asp Tyr Leu Asn Gln Ala Leu Glu
 325 330 335
 Arg Leu Glu Arg Asn Asp Val Arg Tyr Arg Phe Val Val Asp Val Ala
 340 345 350
 Gly Ser Asn Ile Asp Asp Thr Ala Ala
 355 360

<210> 97
 <211> 361
 <212> PRT
 <213> *Festuca arundinacea*

<400> 97
 Met Gly Ser Val Asp Ala Ser Glu Lys Thr Ile Thr Gly Trp Ala Ala
 1 5 10 15
 Arg Asp Thr Thr Gly His Leu Ser Pro Tyr Thr Tyr Thr Leu Arg Arg
 20 25 30
 Thr Gly Ala Glu Asp Val Val Leu Lys Val Leu Tyr Cys Gly Ile Cys
 35 40 45

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His Thr Asp Leu His Gln Thr Lys Asn His Leu Gly Ala Ser Lys Tyr
 50      55      60
Pro Met Val Pro Gly His Glu Val Val Gly Glu Val Val Glu Val Gly
65      70      75      80
Pro Glu Val Ser Lys Tyr Ser Val Gly Asp Val Val Gly Val Gly Val
      85      90      95
Ile Val Gly Cys Cys His Asp Cys Arg Pro Cys Lys Ala Asn Val Glu
      100      105      110
Gln Tyr Cys Asn Lys Lys Ile Trp Ser Tyr Asn Asp Val Tyr Thr Asp
      115      120      125
Gly Lys Pro Thr Gln Gly Gly Phe Ala Ser Ala Met Val Val Asp Gln
130      135      140
Lys Phe Ala Val Lys Ile Pro Ala Gly Leu Ala Pro Glu Gln Ala Ala
145      150      155      160
Pro Leu Leu Cys Ala Gly Val Thr Val Tyr Ser Pro Leu Lys His Phe
      165      170      175
Gly Leu Met Thr Pro Gly Leu Arg Gly Ile Leu Gly Leu Gly Gly
      180      185      190
Val Gly His Met Gly Val Lys Val Ala Lys Ser Met Gly His His Val
195      200      205
Thr Val Ile Ser Ser Ser Asn Lys Lys Arg Ala Glu Ala Met Asp Asp
210      215      220
Leu Gly Ala Asp Ala Tyr Leu Val Ser Ser Asp Glu Ala Gln Met Ala
225      230      235      240
Ala Ala Met Asp Ser Leu Asp Tyr Ile Ile Asp Thr Val Pro Val Lys
      245      250      255
His Pro Leu Glu Pro Tyr Leu Ala Leu Lys Met Asp Gly Lys Leu
      260      265      270
Val Leu Met Gly Val Ile Ala Glu Pro Leu Ser Phe Val Ser Pro Met
275      280      285
Val Met Leu Gly Arg Lys Thr Ile Thr Gly Ser Phe Ile Gly Ser Ile
290      295      300
Glu Glu Thr Glu Glu Val Leu Arg Phe Cys Val Glu Lys Gly Leu Thr
305      310      315      320
Ser Gln Ile Glu Val Val Lys Met Asp Tyr Leu Asn His Ala Leu Glu
      325      330      335
Arg Leu Glu Arg Asn Asp Val Arg Tyr Arg Phe Val Val Asp Val Ala
      340      345      350
Gly Ser Asn Ile Lys Asp Ala Asp Ala
      355      360

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<210> 98

<211> 265

<212> PRT

<213> Lolium perenne

<400> 98

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Met Ala Thr Thr Ala Ala Asp Ala Thr Ala Thr Val Ala Lys Glu Gln
 1      5      10      15
Thr Thr Thr Asn Gly Ala Ala Ser Gly Ala Glu Gln Val Thr Arg His
      20      25      30
Ser Glu Val Gly His Lys Ser Leu Leu Gln Ser Asp Ala Leu Tyr Gln
      35      40      45
Tyr Ile Leu Glu Thr Thr Val Tyr Pro Arg Glu His Glu Cys Met Lys
      50      55      60
Gln Leu Arg Glu Asp Thr Ala Asn His Pro Trp Asn Leu Met Thr Thr
      65      70      75      80
Ser Ala Asp Glu Gly Gln Phe Leu Asn Leu Leu Ile Lys Leu Ile Gly
      85      90      95
Ala Lys Lys Thr Met Glu Ile Gly Val Tyr Thr Gly Tyr Ser Leu Leu
      100      105      110
Ala Thr Ala Leu Ala Ile Pro Glu Asp Gly Thr Ile Leu Ala Met Asp
      115      120      125
Ile Asn Arg Glu Asn Tyr Glu Thr Ile Gly Lys Pro Cys Ile Glu Lys
130      135      140

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Ala Gly Val Ala His Lys Ile Asp Phe Arg Glu Gly Pro Ala Leu Pro
 145 150 155 160
 Val Leu Asp Glu Leu Leu Glu Asp Glu Ala Asn His Gly Thr Phe Asp
 165 170 175
 Phe Val Phe Val Asp Ala Asp Lys Asp Asn Tyr Leu Asn Tyr His Gln
 180 185 190
 Arg Leu Met Lys Leu Val Arg Val Gly Gly Leu Leu Gly Tyr Asp Asn
 195 200 205
 Thr Leu Trp Asn Gly Ser Val Val Leu Pro Ala Asp Ala Pro Met Arg
 210 215 220
 Lys Tyr Ile Arg Tyr Tyr Arg Asp Phe Val Leu Glu Leu Asn Lys Ala
 225 230 235 240
 Leu Ala Ala Asp Asp Arg Val Glu Ile Cys Gln Leu Pro Val Gly Asp
 245 250 255
 Gly Ile Thr Leu Cys Arg Arg Ala Lys
 260 265

<210> 99

<211> 265

<212> PRT

<213> Festuca arundinacea

<400> 99

Met Ala Thr Thr Ala Ala Asp Ala Thr Ala Thr Val Pro Lys Glu Gln
 1 5 10 15
 Pro Ala Thr Asn Gly Ala Ala Ser Gly Ala Glu Gln Val Thr Arg His
 20 25 30
 Ser Glu Val Gly His Lys Ser Leu Leu Gln Ser Asp Ala Leu Tyr Gln
 35 40 45
 Tyr Ile Leu Glu Thr Thr Val Tyr Pro Arg Glu His Glu Cys Met Lys
 50 55 60
 Gln Leu Arg Glu Asp Thr Ala Asn His Pro Trp Asn Leu Met Thr Thr
 65 70 75 80
 Ser Ala Asp Glu Gly Gln Phe Leu Asn Leu Leu Ile Lys Leu Ile Gly
 85 90 95
 Ala Lys Lys Thr Met Glu Ile Gly Val Tyr Thr Gly Tyr Ser Leu Leu
 100 105 110
 Ala Thr Ala Leu Ala Ile Pro Glu Asp Gly Thr Ile Leu Ala Met Asp
 115 120 125
 Ile Asn Arg Glu Asn Tyr Glu Thr Ile Gly Lys Pro Cys Ile Glu Lys
 130 135 140
 Ala Gly Val Ala His Lys Ile Asp Phe Arg Glu Gly Pro Ala Leu Pro
 145 150 155 160
 Val Leu Asp Glu Leu Leu Glu Asp Glu Ala Asn His Gly Ser Phe Asp
 165 170 175
 Phe Val Phe Val Asp Ala Asp Lys Asp Asn Tyr Leu Asn Tyr His Gln
 180 185 190
 Arg Leu Met Lys Leu Val Arg Val Gly Gly Leu Ile Gly Tyr Asp Asn
 195 200 205
 Thr Leu Trp Asn Gly Ser Val Val Leu Pro Ala Asp Ala Pro Met Arg
 210 215 220
 Lys Tyr Ile Arg Tyr Tyr Arg Asp Phe Val Leu Glu Leu Asn Lys Ala
 225 230 235 240
 Leu Ala Ala Asp Asp Arg Val Glu Ile Cys Gln Leu Pro Val Gly Asp
 245 250 255
 Gly Ile Thr Leu Cys Arg Arg Ala Lys
 260 265

<210> 100

<211> 363

<212> PRT

<213> Lolium perenne

<400> 100

Met Thr Val Val Glu Val Leu Ala Ala Gly Asp Ala Ala Ala Ala Ala
 1 5 10 15

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Val Ala Arg Pro Ala Gly Asn Gly Gln Thr Val Cys Val Thr Gly Ala
      20      25
Ala Gly Tyr Ile Ala Ser Trp Leu Val Lys Leu Leu Leu Glu Lys Gly
      35      40      45
Tyr Thr Val Lys Gly Thr Val Arg Asn Pro Asp Asp Pro Lys Asn Ala
      50      55      60
His Leu Arg Ala Leu Asp Gly Ala Ala Asp Arg Leu Val Leu Cys Lys
      65      70      75      80
Ala Asp Leu Leu Asp Tyr Asp Ala Ile Arg Arg Ala Ile Asp Gly Cys
      85      90      95
His Gly Val Phe His Thr Ala Ser Pro Val Thr Asp Asp Pro Glu Gln
      100      105      110
Met Val Glu Pro Ala Val Arg Gly Thr Gln Tyr Val Ile Asp Ala Ala
      115      120      125
Ala Glu Ala Gly Thr Val Arg Arg Met Val Leu Thr Ser Ser Ile Gly
      130      135      140
Ala Val Thr Met His Pro Asn Arg Gly Pro Asp Val Val Val Asp Glu
      145      150      155      160
Ser Cys Trp Ser Asp Leu Asp Phe Cys Lys Lys Thr Arg Asn Trp Tyr
      165      170      175
Cys Tyr Gly Lys Ala Val Ala Glu Gln Ala Ala Ser Glu Leu Ala Arg
      180      185      190
Gln Arg Gly Val Asp Leu Val Val Val Asn Pro Val Leu Val Ile Gly
      195      200      205
Pro Leu Leu Gln Pro Thr Val Asn Ala Ser Ile Gly His Ile Leu Lys
      210      215      220
Tyr Leu Asp Gly Ser Ala Ser Lys Phe Ala Asn Ala Val Gln Ala Tyr
      225      230      235      240
Val Asp Val Arg Asp Val Ala Asp Ala His Leu Arg Val Phe Glu Cys
      245      250      255
Ala Ala Ala Ser Gly Arg His Leu Cys Ala Glu Arg Val Leu His Arg
      260      265      270
Glu Asp Val Val Arg Ile Leu Ala Lys Leu Phe Pro Glu Tyr Pro Val
      275      280      285
Pro Thr Arg Cys Ser Asp Glu Ala Asn Pro Arg Lys Gln Pro Tyr Lys
      290      295      300
Met Ser Asn Gln Lys Leu Gln Asp Leu Gly Leu Glu Phe Arg Pro Val
      305      310      315      320
Ser Gln Ser Leu Tyr Glu Thr Val Lys Ser Leu Gln Glu Lys Gly His
      325      330      335
Leu Pro Val Leu Ser Glu Gln Ala Glu Ala Asp Lys Glu Thr Leu Ala
      340      345      350
Ala Glu Leu Gln Ala Gly Val Thr Ile Arg Ala
      355      360

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<210> 101

<211> 342

<212> PRT

<213> Festuca arundinacea

<400> 101

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Met Thr Val Val Asp Ala Ala Ala Pro Gln Leu Pro Gly His Gly Gln
  1      5      10      15
Thr Val Cys Val Thr Gly Ala Ala Gly Tyr Ile Ala Ser Gly Leu Val
      20      25      30
Lys Leu Leu Leu Glu Arg Gly Tyr Val Lys Gly Thr Val Arg Asn
      35      40      45
Pro Asp Asp Pro Lys Asn Ala His Leu Lys Ala Leu Asp Gly Ala Thr
      50      55      60
Glu Arg Leu Ile Leu Cys Lys Ala Asp Leu Leu Asp Tyr Asp Ala Ile
      65      70      75      80
Cys Ala Ala Val Glu Gly Cys His Gly Val Phe His Thr Ala Ser Pro
      85      90      95
Val Thr Asp Asp Pro Glu Gln Met Val Glu Pro Ala Val Arg Gly Thr
      100      105      110

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Glu Tyr Val Ile Asn Ala Ala Ala Asp Ala Gly Thr Val Arg Arg Val
 115 120 125
 Val Phe Thr Ser Ser Ile Gly Ala Ile Thr Met Asp Pro Asn Arg Gly
 130 135 140
 Pro Asp Val Val Val Asn Glu Ser Cys Trp Ser Asp Leu Glu Phe Cys
 145 150 155 160
 Lys Lys Thr Lys Asn Trp Tyr Cys Tyr Gly Lys Ala Val Ala Glu Gln
 165 170 175
 Ala Ala Trp Glu Ala Ala Arg Lys Arg Gly Ile Asp Leu Val Val Val
 180 185 190
 Asn Pro Val Leu Val Val Gly Pro Leu Leu Gln Pro Thr Val Asn Ala
 195 200 205
 Ser Ala Ala His Ile Leu Lys Tyr Leu Asp Gly Ser Ala Lys Lys Tyr
 210 215 220
 Ala Asn Ala Val Gln Ser Tyr Val Asp Val Arg Asp Val Ala Gly Ala
 225 230 235 240
 His Ile Arg Val Phe Glu Ala Pro Glu Ala Ser Gly Arg Tyr Leu Cys
 245 250 255
 Ala Glu Arg Val Leu His Arg Gly Asp Val Val Gln Ile Leu Ser Lys
 260 265 270
 Leu Phe Pro Glu Tyr Pro Val Pro Thr Arg Cys Ser Asp Glu Val Asn
 275 280 285
 Pro Arg Lys Gln Pro Tyr Lys Met Ser Asn Gln Lys Leu Gln Asp Leu
 290 295 300
 Gly Leu Gln Phe Thr Pro Val Asn Asp Ser Leu Tyr Glu Thr Val Lys
 305 310 315 320
 Ser Leu Gln Glu Lys Gly His Leu Leu Val Pro Ser Lys Pro Glu Gly
 325 330 335
 Leu Asn Gly Val Thr Ala
 340

<210> 102

<211> 360

<212> PRT

<213> Festuca arundinacea

<400> 102

Met Gly Ser Thr Ala Ala Asp Met Ala Ala Ser Ala Asp Gln Glu Ala
 1 5 10 15
 Cys Met Phe Ala Leu Gln Leu Ala Ser Ser Ser Ile Leu Pro Met Thr
 20 25 30
 Leu Lys Asn Ala Ile Glu Leu Gly Leu Leu Glu Ile Leu Val Ala Ala
 35 40 45
 Gly Gly Lys Ser Leu Thr Pro Thr Glu Val Ala Ala Lys Leu Pro Ser
 50 55 60
 Ala Ala Asn Pro Glu Ala Pro Asp Met Val Asp Arg Met Leu Arg Leu
 65 70 75 80
 Leu Ala Ser Tyr Asn Val Val Thr Cys Leu Val Glu Glu Gly Lys Asp
 85 90 95
 Gly Arg Leu Ser Arg Ser Tyr Gly Ala Ala Pro Val Cys Lys Phe Leu
 100 105 110
 Thr Pro Asn Glu Asp Gly Val Ser Met Ala Ala Leu Ala Leu Met Asn
 115 120 125
 Gln Asp Lys Val Leu Met Glu Ser Trp Tyr Tyr Leu Lys Asp Ala Val
 130 135 140
 Leu Asp Gly Gly Ile Pro Phe Asn Lys Ala Tyr Gly Met Ser Ala Phe
 145 150 155 160
 Glu Tyr His Gly Thr Asp Pro Arg Phe Asn Arg Val Phe Asn Glu Gly
 165 170 175
 Met Lys Asn His Ser Ile Ile Ile Thr Lys Lys Leu Leu Glu Leu Tyr
 180 185 190
 His Gly Phe Gln Gly Leu Gly Thr Leu Val Asp Val Gly Gly Gly Val
 195 200 205
 Gly Ala Thr Val Ala Ala Ile Ala Ala His Tyr Pro Ala Ile Lys Gly
 210 215 220

Val Asn Phe Asp Leu Pro His Val Ile Ser Glu Ala Pro Gln Phe Pro
 225 230 235 240
 Gly Val Thr His Val Gly Gly Asp Met Phe Lys Glu Val Pro Ser Gly
 245 250 255
 Asp Ala Ile Leu Met Lys Trp Ile Leu His Asp Trp Ser Asp Gln His
 260 265 270
 Cys Ala Thr Leu Leu Lys Asn Cys Tyr Asp Ala Leu Pro Ala His Gly
 275 280 285
 Lys Val Val Leu Val Glu Cys Ile Leu Pro Val Asn Pro Glu Ala Lys
 290 295 300
 Pro Ser Ser Gln Gly Val Phe His Val Asp Met Ile Met Leu Ala His
 305 310 315 320
 Asn Pro Gly Gly Arg Glu Arg Tyr Glu Arg Glu Phe Glu Ala Leu Ala
 325 330 335
 Arg Gly Ala Gly Phe Thr Gly Val Lys Ser Thr Tyr Ile Tyr Ala Asn
 340 345 350
 Ala Trp Ala Ile Glu Phe Thr Lys
 355 360

<210> 103

<211> 360

<212> PRT

<213> FLolium perenne

<400> 103

Met Gly Ser Thr Ala Ala Asp Met Ala Ala Ser Ala Asp Glu Asp Ala
 1 5 10 15
 Cys Met Phe Ala Leu Gln Leu Ala Ser Ser Ser Val Leu Pro Met Thr
 20 25 30
 Leu Lys Asn Ala Ile Glu Leu Gly Leu Leu Glu Ile Leu Val Ala Ala
 35 40 45
 Gly Gly Lys Ser Leu Thr Pro Thr Glu Val Ala Ala Lys Leu Pro Ser
 50 55 60
 Ala Ala Asn Pro Glu Ala Pro Asp Met Val Asp Arg Ile Leu Arg Leu
 65 70 75 80
 Leu Ala Ser Tyr Asn Val Val Thr Cys Leu Val Glu Glu Gly Lys Asp
 85 90 95
 Gly Arg Leu Ser Arg Ser Tyr Gly Ala Ala Pro Val Cys Lys Phe Leu
 100 105 110
 Thr Pro Asn Glu Asp Gly Val Ser Met Ala Ala Leu Ala Leu Met Asn
 115 120 125
 Gln Asp Lys Val Leu Met Glu Ser Trp Tyr Tyr Leu Lys Asp Ala Val
 130 135 140
 Leu Asp Gly Gly Ile Pro Phe Asn Lys Ala Tyr Gly Met Ser Ala Phe
 145 150 155 160
 Glu Tyr His Gly Thr Asp Pro Arg Phe Asn Arg Val Phe Asn Glu Gly
 165 170 175
 Met Lys Asn His Ser Ile Ile Ile Thr Lys Lys Leu Leu Glu Leu Tyr
 180 185 190
 His Gly Phe Glu Gly Leu Gly Ser Leu Val Asp Val Gly Gly Gly Val
 195 200 205
 Gly Ala Thr Val Ala Ala Ile Ala Ala His Tyr Pro Thr Ile Lys Gly
 210 215 220
 Val Asn Phe Asp Leu Pro His Val Ile Ser Glu Ala Pro Gln Phe Pro
 225 230 235 240
 Gly Val Thr His Val Gly Gly Asp Met Phe Lys Glu Val Pro Ser Gly
 245 250 255
 Asp Ala Ile Leu Met Lys Trp Ile Leu His Asp Trp Ser Asp Gln His
 260 265 270
 Cys Ala Thr Leu Leu Lys Asn Cys Tyr Asp Ala Leu Pro Ala His Gly
 275 280 285
 Lys Val Val Leu Val Glu Cys Ile Leu Pro Val Asn Pro Glu Ala Asn
 290 295 300
 Pro Ser Ser Gln Gly Val Phe His Val Asp Met Ile Met Leu Ala His
 305 310 315 320

Asn	Pro	Gly	Gly	Arg	Glu	Arg	Tyr	Glu	Arg	Glu	Phe	Gln	Ala	Leu	Ala
				325					330					335	
Arg	Gly	Ala	Gly	Phe	Thr	Gly	Val	Lys	Ser	Thr	Tyr	Ile	Tyr	Ala	Asn
			340					345						350	
Ala	Trp	Ala	Ile	Glu	Phe	Thr	Lys								
		355					360								

<210> 104

$\langle 211 \rangle \quad 360^\circ$

<212> PRT

<213> Festuca arundinacea

<400> 104

Met 1	Gly	Ser	Thr	Ala 5	Ala	Asp	Met	Thr	Ala 10	Ser	Ala	Asp	Glu 15	Glu	Ala
Cys	Met	Phe	Ala 20	Leu	Gln	Leu	Ala 25	Ser	Ser	Ser	Ile	Leu 30	Pro	Met	Thr
Leu	Lys	Asn 35	Ala	Ile	Glu	Leu	Gly 40	Leu	Leu	Glu	Ile	Leu 45	Val	Ala	Ala
Gly	Gly	Lys 50	Ser	Leu	Thr	Pro 55	Thr	Glu	Val	Ala	Ala 60	Lys	Leu	Pro	Ser
Ala 65	Ala	Asn	Pro	Glu 70	Ala	Pro	Asp	Met	Val	Asp 75	Arg	Met	Leu	Arg	Leu 80
Leu	Ala	Ser	Tyr	Asn 85	Val	Val	Ser	Cys	Leu 90	Val	Glu	Glu	Gly 95	Lys	Asp
Gly	Arg	Leu 100	Ser	Arg	Asn	Tyr	Gly	Ala 105	Ala	Pro	Val	Cys	Lys 110	Phe	Leu
Thr	Pro	Asn 115	Glu	Asp	Gly	Val	Ser	Met 120	Ala	Ala	Leu	Ala 125	Leu	Met	Asn
Gln	Asp	Lys 130	Val	Leu	Met	Glu 135	Ser	Trp	Tyr	Tyr	Leu 140	Lys	Asp	Ala	Val
Leu 145	Asp	Gly	Gly	Ile 150	Pro	Phe	Asn	Lys	Ala	Tyr 155	Gly	Met	Ser	Ala	Phe 160
Glu	Tyr	His	Gly	Thr 165	Asp	Pro	Arg	Phe	Asn 170	Arg	Val	Phe	Asn 175	Glu	Gly
Met	Lys	Asn 180	His	Ser	Ile	Ile	Ile	Thr 185	Lys	Lys	Leu	Leu 190	Glu	Leu	Tyr
Asp	Gly	Phe 195	Gln	Gly	Leu	Gly	Thr 200	Leu	Val	Asp	Val	Gly 205	Gly	Gly	Val
Gly	Ala	Thr 210	Val	Ala 215	Ala	Ile	Thr	Ala	His	Tyr	Pro 220	Ala	Ile	Lys	Gly
Val 225	Asn	Phe	Asp	Leu 230	Pro	His	Val	Ile	Ser	Glu 235	Ala	Pro	Pro	Phe	Pro 240
Gly	Val	Thr	His	Val 245	Gly	Gly	Asp	Met	Phe 250	Lys	Lys	Val	Pro	Ser	Gly
Asp	Ala	Ile	Met	Met 260	Lys	Trp	Ile	Leu 265	His	Asp	Trp	Ser	Asp 270	Gln	His
Cys	Ala	Thr 275	Leu	Leu	Lys	Asn	Cys 280	Tyr	Asp	Ala	Leu	Pro 285	Ala	His	Gly
Lys	Val	Val 290	Leu	Val	Glu	Cys 295	Ile	Leu	Pro	Val 300	Asn	Pro	Glu	Ala	Lys
Pro 305	Ser	Ser	Gln	Gly 310	Val	Phe	His	Val	Asp	Met 315	Ile	Met	Leu	Ala	His 320
Asn	Pro	Gly	Gly	Arg 325	Glu	Arg	Tyr	Glu	Arg 330	Glu	Phe	Glu	Ala 335	Leu	Ala
Arg	Gly	Ala	Gly	Phe 340	Ala	Gly	Val	Lys 345	Ser	Thr	Tyr	Ile	Tyr 350	Ala	Asn
Ala	Trp	Ala 355	Ile	Glu	Phe	Thr	Lys 360								

<210> 105

<211> 361

<212> PRT

<213> Lolium perenne

<400> 105

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Met Gly Ser Thr Ala Ala Glu Ile Ala Ala Ser Ala Asp Glu Glu Ala
 1          5          10          15
Cys Leu Tyr Ala Leu Gln Leu Gly Ser Ser Ser Ile Leu Pro Met Thr
 20          25          30
Leu Lys Asn Thr Ile Glu Leu Gly Leu Leu Glu Thr Leu Met Ala Ala
 35          40          45
Gly Gly Lys Ser Leu Thr Pro Thr Glu Val Ala Ala Lys Leu Pro Cys
 50          55          60
Ala Ala Lys Asn Pro Glu Ala Pro Asp Met Val Asp Arg Met Leu Arg
 65          70          75          80
Leu Leu Ala Ser Tyr Asn Leu Val Ser Cys Leu Val Glu Glu Gly Thr
 85          90          95
Asp Gly Arg Leu Ser Arg Arg Tyr Gly Ala Ala Pro Val Cys Lys Phe
100          105          110
Leu Thr Pro Asn Glu Asp Gly Val Ser Met Ala Ala Leu Ala Leu Met
115          120          125
Asn Gln Asp Lys Val Leu Met Glu Ser Trp Tyr Tyr Leu Lys Asp Ala
130          135          140
Val Leu Asp Gly Gly Ile Pro Phe Asn Lys Ala Tyr Gly Met Ser Ala
145          150          155          160
Phe Glu Tyr His Gly Thr Asp Leu Arg Phe Asn Arg Val Phe Asn Glu
165          170          175
Ala Met Lys Asn Asn Ser Ile Ile Ile Thr Lys Lys Leu Leu Gln Leu
180          185          190
Tyr Asp Gly Phe Gln Gly Leu Gly Thr Leu Val Asp Val Gly Gly Gly
195          200          205
Val Gly Ala Thr Val Ala Ala Ile Thr Ala His Tyr Pro Thr Ile Lys
210          215          220
Gly Ile Asn Phe Asp Leu Pro His Val Ile Ser Glu Ala Pro Pro Phe
225          230          235          240
Pro Gly Val Thr His Ile Gly Gly Asp Met Phe Lys Lys Val Pro Ser
245          250          255
Gly Asp Ala Ile Leu Met Lys Trp Ile Leu His Asp Trp Ser Asp Gln
260          265          270
His Cys Ala Thr Leu Leu Lys Asn Cys Tyr Asp Ala Leu Pro Val His
275          280          285
Gly Lys Val Val Leu Val Glu Cys Ile Leu Pro Val Asn Pro Glu Ala
290          295          300
Lys Pro Ser Ser Gln Gly Val Phe His Val Asp Met Ile Met Leu Ala
305          310          315          320
His Asn Pro Gly Gly Arg Glu Arg Tyr Glu Arg Glu Tyr Glu Ala Leu
325          330          335
Ala Arg Gly Ala Gly Phe Ala Gly Phe Lys Ser Thr Tyr Ile Tyr Ala
340          345          350
Asn Ala Trp Ala Ile Glu Phe Thr Lys
355          360

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<210> 106

<211> 532

<212> PRT

<213> Lolium perenne

<400> 106

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Met Val Gly Phe Ala Lys Ile Ala Met Glu Trp Ile Gln Asp Pro Leu
 1          5          10          15
Ser Trp Leu Phe Ile Ala Ser Val Val Phe Val Val Leu Gln Arg Arg
 20          25          30
Arg Arg Gly Asn Val Ala Pro Phe Pro Pro Gly Pro Lys Pro Leu Pro
 35          40          45
Ile Val Gly Asn Met Ser Met Met Asp Gln Leu Thr His Arg Gly Leu
 50          55          60
Ala Ala Leu Ala Lys Glu Tyr Gly Gly Leu Leu His Ile Arg Leu Gly
 65          70          75          80
Lys Leu His Thr Phe Ala Val Ser Thr Pro Glu Tyr Ala Arg Glu Val
 85          90          95

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Leu Gln Val Gln Asp Gly Ala Phe Ser Asn Arg Pro Ala Thr Ile Ala
 100 105 110
 Ile Ala Tyr Leu Thr Tyr Asp Arg Ala Asp Met Ala Phe Ala His Tyr
 115 120 125
 Gly Pro Phe Trp Arg Gln Met Arg Lys Leu Cys Val Met Lys Leu Phe
 130 135 140
 Ser Arg Arg Arg Pro Glu Thr Trp Leu Ala Val Arg Asp Glu Ser Ala
 145 150 155 160
 Ala Leu Val Arg Ala Val Ala Arg Arg Thr Gly Glu Ser Val Asp Leu
 165 170 175
 Gly Glu Leu Ile Phe Lys Leu Thr Lys Asn Val Ile Phe Arg Ala Ala
 180 185 190
 Phe Gly Ala Gly Ala Val Ala Ala Asp Ala Glu Glu Gly Asp Gly Ala
 195 200 205
 Gly Lys Gln Asp Glu Phe Ile Ala Ile Leu Gln Glu Phe Ser Lys Leu
 210 215 220
 Phe Gly Ala Phe Asn Ile Gly Asp Phe Ile Pro Trp Leu Ser Trp Ala
 225 230 235 240
 Asp Pro Gln Gly Ile Asn Val Arg Leu Arg Ala Ala Arg Asn Ala Leu
 245 250 255
 Asp Glu Phe Ile Asp Lys Ile Ile Asp Glu His Met Glu Arg Gly Lys
 260 265 270
 Asn Pro Asp Ala Asp Ala Asp Met Val Asp Asp Met Leu Ala Phe
 275 280 285
 Leu Pro Glu Ala Lys Pro Lys Lys Gly Ala Ala Gly Asp Gly Val Asp
 290 295 300
 Asp Leu Gln Asn Thr Leu Arg Leu Thr Arg Asp Asn Ile Lys Ala Ile
 305 310 315 320
 Ile Met Asp Val Met Phe Gly Gly Thr Glu Thr Val Ala Ser Ala Ile
 325 330 335
 Glu Trp Ala Met Ala Glu Met Met His Ser Pro Asp Asp Leu Arg Arg
 340 345 350
 Leu Gln Gln Glu Leu Val Asp Val Val Gly Leu Asp Arg Asn Val Asp
 355 360 365
 Glu Ser Asp Leu Asp Lys Leu Pro Phe Leu Lys Cys Val Ile Lys Glu
 370 375 380
 Thr Leu Arg Leu His Pro Pro Ile Pro Leu Leu His Glu Thr Ala
 385 390 395 400
 Glu Asp Cys Val Val Gly Gly Tyr Ser Val Pro Arg Gly Ser Arg Val
 405 410 415
 Met Ile Asn Val Tyr Ala Ile Gly Arg Asp Arg Arg Ala Trp Lys Asp
 420 425 430
 Ala Asp Val Phe Arg Pro Ser Arg Phe Val Gln Gly Glu Gly Glu Ala
 435 440 445
 Ala Gly Leu Asp Phe Lys Gly Gly Cys Phe Glu Phe Leu Pro Phe Gly
 450 455 460
 Ser Gly Arg Arg Ser Cys Pro Gly Met Ala Leu Gly Leu Tyr Ala Leu
 465 470 475 480
 Glu Leu Ala Val Ala Gln Leu Ala His Gly Phe Ser Trp Glu Leu Pro
 485 490 495
 Asp Gly Met Lys Pro Ser Glu Leu Asp Met Ser Asp Val Phe Gly Leu
 500 505 510
 Thr Ala Pro Arg Ala Thr Arg Leu Phe Ala Val Pro Thr Pro Arg Leu
 515 520 525
 Ala Cys Thr Gln
 530

<210> 107

<211> 542

<212> PRT

<213> Festuca arundinacea

<400> 107

Met Val Gly Phe Ala Lys Ile Ala Met Glu Trp Leu Gln Glu Pro Leu
 1 5 10 15

Ser Trp Leu Phe Ile Ala Ser Val Val Phe Val Val Leu Gln Arg Arg
 20 25 30
 Arg Arg Gly Asn Val Ala Pro Phe Pro Pro Gly Pro Lys Pro Leu Pro
 35 40 45
 Ile Val Gly Asn Met Ser Met Met Asp Gln Leu Thr His Arg Gly Leu
 50 55 60
 Ala Ala Leu Ala Lys Glu Tyr Gly Gly Leu Leu His Ile Arg Leu Gly
 65 70 75 80
 Lys Leu His Ala Phe Ala Val Ser Thr Pro Glu Tyr Ala Arg Glu Val
 85 90 95
 Leu Gln Val Gln Asp Gly Ala Phe Ser Asn Arg Pro Ala Thr Ile Ala
 100 105 110
 Ile Ala Tyr Leu Thr Tyr Asp Arg Ala Asp Met Ala Phe Ala His Tyr
 115 120 125
 Gly Pro Phe Trp Arg Gln Met Arg Lys Leu Cys Val Met Lys Leu Phe
 130 135 140
 Ser Arg Arg Arg Pro Glu Thr Trp Leu Ala Val Arg Asp Glu Ser Ala
 145 150 155 160
 Ala Leu Val Arg Ala Val Ala Arg Arg Ser Gly Glu Ser Val Asp Leu
 165 170 175
 Gly Glu Leu Ile Phe Lys Leu Thr Lys Asn Val Ile Phe Arg Ala Ala
 180 185 190
 Phe Gly Ala Gly Ala Val Ala Gly Asp Gly Asp Gly Asp Gly Ala Gly
 195 200 205
 Lys Gln Asp Glu Phe Ile Ala Ile Leu Gln Glu Phe Ser Lys Leu Phe
 210 215 220
 Gly Ala Phe Asn Ile Gly Asp Phe Ile Pro Trp Leu Ser Trp Ala Asp
 225 230 235 240
 Pro Gln Gly Ile Asn Val Arg Leu Arg Ala Ala Arg Ala Ala Leu Asp
 245 250 255
 Glu Phe Ile Asp Lys Ile Ile Asp Glu His Met Glu Arg Gly Lys Asn
 260 265 270
 Pro Asp Asp Ala Asp Ala Asp Met Val Asp Asp Met Leu Ala Phe Leu
 275 280 285
 Pro Glu Thr Lys Pro Lys Lys Gly Ala Ala Gly Asp Gly Val Asp Asp
 290 295 300
 Leu Gln Asn Thr Leu Arg Leu Thr Arg Asp Asn Ile Lys Ala Ile Ile
 305 310 315 320
 Met Asp Val Met Phe Gly Gly Thr Glu Thr Val Ala Ser Ala Ile Glu
 325 330 335
 Trp Ala Met Ala Glu Met Met His Ser Pro Gly Asp Leu Arg Arg Leu
 340 345 350
 Gln Gln Glu Leu Ala Asp Val Val Gly Leu Asp Arg Asn Val Asp Glu
 355 360 365
 Ser Asp Leu Asp Lys Leu Pro Phe Leu Lys Cys Val Ile Lys Glu Thr
 370 375 380
 Leu Arg Leu His Pro Pro Ile Pro Leu Leu Leu His Glu Thr Ala Glu
 385 390 395 400
 Asp Cys Ile Val Gly Gly Tyr Ser Val Pro Arg Gly Ser Arg Val Met
 405 410 415
 Ile Asn Val Tyr Ala Ile Gly Arg Asp Arg Lys Ala Trp Lys Asp Ala
 420 425 430
 Asp Val Phe Arg Pro Ser Arg Phe Val Gln Gly Glu Gly Glu Ala Ala
 435 440 445
 Gly Leu Asp Phe Lys Gly Gly Cys Phe Glu Phe Leu Pro Phe Gly Ser
 450 455 460
 Gly Arg Arg Ser Cys Pro Gly Met Ala Leu Gly Leu Tyr Ala Leu Glu
 465 470 475 480
 Leu Ala Val Ala Gln Leu Ala His Gly Phe Ser Trp Glu Leu Pro Asp
 485 490 495
 Gly Met Lys Pro Ser Glu Leu Asp Met Ser Asp Val Phe Gly Leu Thr
 500 505 510
 Ala Pro Arg Ala Thr Arg Leu Phe Ala Val Pro Thr Pro Arg Leu Ala
 515 520 525
 Cys Thr Gln Leu Leu Gly Ala Asp Asp Ala Gly Arg Gln Ala
 530 535 540

<210> 108
 <211> 711
 <212> PRT
 <213> Lolium perenne

<400> 108
 Met Glu Ser Glu Asn Val Ala Ala Asn Gly Asp Gly Leu Cys Val Ala
 1 5 10 15
 Gln Pro Ala Arg Ala Asp Pro Leu Asn Trp Gly Lys Ala Ala Glu Glu
 20 25 30
 Leu Ser Gly Ser His Leu Asp Ala Val Lys Arg Met Val Glu Glu Tyr
 35 40 45
 Arg Arg Pro Val Val Thr Met Glu Gly Ala Ser Leu Thr Ile Ala Met
 50 55 60
 Val Ala Ala Val Ala Ala Gly Ala Asp Thr Arg Val Glu Leu Asp Glu
 65 70 75 80
 Ser Ala Arg Gly Arg Val Lys Glu Ser Ser Asp Trp Val Met Asn Ser
 85 90 95
 Met Ala Asn Gly Thr Asp Ser Tyr Gly Val Thr Thr Gly Phe Gly Ala
 100 105 110
 Thr Ser His Arg Arg Thr Lys Glu Gly Gly Ala Leu Gln Arg Glu Leu
 115 120 125
 Ile Arg Phe Leu Asn Ala Gly Ala Phe Gly Thr Gly Ser Asp Gly His
 130 135 140
 Val Leu Pro Ala Ala Thr Thr Arg Ala Ala Met Leu Val Arg Val Asn
 145 150 155 160
 Thr Leu Leu Gln Gly Tyr Ser Gly Ile Arg Phe Glu Ile Leu Glu Thr
 165 170 175
 Val Ala Thr Leu Leu Asn Ala Asn Val Thr Pro Cys Leu Pro Leu Arg
 180 185 190
 Gly Thr Ile Thr Ala Ser Gly Asp Leu Val Pro Leu Ser Tyr Ile Ala
 195 200 205
 Gly Leu Val Thr Gly Arg Pro Asn Ser Val Ala Thr Ala Pro Asp Gly
 210 215 220
 Thr Lys Val Asn Ala Ala Glu Ala Phe Lys Ile Ala Gly Ile Gln His
 225 230 235 240
 Gly Phe Phe Glu Leu Gln Pro Lys Glu Gly Leu Ala Met Val Asn Gly
 245 250 255
 Thr Ala Val Gly Ser Gly Leu Ala Ser Met Val Leu Phe Glu Ala Asn
 260 265 270
 Ile Leu Gly Ile Leu Ala Glu Val Leu Ser Ala Val Phe Cys Glu Val
 275 280 285
 Met Asn Gly Lys Pro Glu Tyr Thr Asp His Leu Thr His Lys Leu Lys
 290 295 300
 His His Pro Gly Gln Ile Glu Ala Ala Ala Ile Met Glu His Ile Leu
 305 310 315 320
 Glu Gly Ser Ser Tyr Met Met Leu Ala Lys Lys Leu Gly Glu Leu Asp
 325 330 335
 Pro Leu Met Lys Pro Lys Gln Asp Arg Tyr Ala Leu Arg Thr Ser Pro
 340 345 350
 Gln Trp Leu Gly Pro Gln Ile Glu Val Ile Arg Ala Ala Thr Lys Ser
 355 360 365
 Ile Glu Arg Glu Ile Asn Ser Val Asn Asp Asn Pro Leu Ile Asp Val
 370 375 380
 Ser Arg Gly Lys Ala Ile His Gly Gly Asn Phe Gln Gly Thr Pro Ile
 385 390 395 400
 Gly Val Ser Met Asp Asn Thr Arg Leu Ala Ile Ala Ala Ile Gly Lys
 405 410 415
 Leu Met Phe Ala Gln Phe Ser Glu Leu Val Asn Asp Phe Tyr Asn Asn
 420 425 430
 Gly Leu Pro Ser Asn Leu Ser Gly Gly Arg Asn Pro Ser Leu Asp Tyr
 435 440 445
 Gly Phe Lys Gly Ala Glu Ile Ala Met Ala Ser Tyr Cys Ser Glu Leu
 450 455 460

Gln Phe Leu Gly Asn Pro Val Thr Asn His Val Gln Ser Ala Glu Gln
 465 470 475 480
 His Asn Gln Asp Val Asn Ser Leu Gly Leu Ile Ser Ala Arg Lys Thr
 485 490 495
 Ser Glu Ala Ile Asp Ile Leu Lys Leu Met Ser Ser Thr Phe Leu Val
 500 505 510
 Ala Leu Cys Gln Ala Ile Asp Leu Arg His Leu Glu Glu Asn Val Lys
 515 520 525
 Asn Ala Val Lys Asn Cys Val Lys Met Val Ala Arg Lys Thr Leu Ser
 530 535 540
 Thr Asn Asp Ser Gly His Leu His Ser Ala Arg Phe Cys Glu Lys Asp
 545 550 555 560
 Leu Leu Leu Thr Ile Asp Arg Glu Ala Val Phe Ala Tyr Ala Asp Asp
 565 570 575
 Pro Cys Ser Ala Asn Tyr Pro Leu Met Gln Lys Met Arg Ala Val Leu
 580 585 590
 Val Glu His Ala Leu Ala Asn Gly Glu Ala Glu Arg Asp Val Gln Thr
 595 600 605
 Ser Val Phe Ala Lys Leu Ala Ala Phe Glu Gln Glu Leu Arg Ala Val
 610 615 620
 Leu Pro Arg Glu Val Glu Ser Ala Arg Cys Ala Val Glu Asn Gly Thr
 625 630 635 640
 Ala Ala Gln Gln Asn Arg Ile Thr Glu Cys Arg Ser Tyr Pro Leu Tyr
 645 650 655
 Arg Phe Val Arg Lys Glu Leu Gly Thr Glu Tyr Leu Thr Gly Glu Lys
 660 665 670
 Thr Arg Ser Pro Gly Glu Glu Val Asp Lys Val Phe Val Ala Met Asn
 675 680 685
 Gln Gly Lys His Ile Asp Ala Leu Leu Glu Cys Leu Lys Glu Trp Asn
 690 695 700
 Gly Glu Pro Leu Pro Ile Cys
 705 710

<210> 109

<211> 713

<212> PRT

<213> Festuca arundinacea

<400> 109

Met Glu Cys Glu Asn Gly His Val Ala Ala Asn Gly Asp Gly Leu Cys
 1 5 10 15
 Val Ala Gln Pro Ala Arg Ala Asp Pro Leu Asn Trp Gly Lys Ala Ala
 20 25 30
 Glu Glu Leu Ser Gly Ser His Leu Asp Ala Val Lys Arg Met Val Glu
 35 40 45
 Glu Tyr Arg Arg Pro Val Val Thr Met Glu Gly Ala Ser Leu Thr Ile
 50 55 60
 Ala Met Val Ala Ala Val Ala Ala Gly Ala Asp Thr Arg Val Glu Leu
 65 70 75 80
 Asp Glu Ser Ala Arg Gly Arg Val Lys Glu Ser Ser Asp Trp Val Met
 85 90 95
 Asn Ser Met Ala Asn Gly Thr Asp Ser Tyr Gly Val Thr Thr Gly Phe
 100 105 110
 Gly Ala Thr Ser His Arg Arg Thr Lys Glu Gly Gly Ala Leu Gln Arg
 115 120 125
 Glu Leu Ile Arg Phe Leu Asn Ala Gly Ala Phe Gly Thr Gly Ser Asp
 130 135 140
 Gly His Val Leu Pro Ala Ala Thr Thr Arg Ala Ala Met Leu Val Arg
 145 150 155 160
 Val Asn Thr Leu Leu Gln Gly Tyr Ser Gly Ile Arg Phe Glu Ile Leu
 165 170 175
 Glu Thr Ile Ala Thr Leu Leu Asn Ala Asn Val Thr Pro Cys Leu Pro
 180 185 190
 Tyr Arg Gly Thr Ile Thr Ala Ser Gly Asp Leu Val Pro Leu Ser Tyr
 195 200 205

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Ile Ala Gly Leu Val Thr Gly Arg Pro Asn Ser Val Ala Thr Ala Pro
210                215                220
Asp Gly Ser Lys Val Asn Ala Ala Glu Ala Phe Lys Ile Ala Gly Ile
225                230                235                240
Gln His Gly Phe Phe Glu Leu Gln Pro Lys Glu Gly Leu Ala Met Val
                245                250                255
Asn Gly Thr Ala Val Gly Ser Gly Leu Ala Ser Ile Val Leu Phe Glu
                260                265                270
Ala Asn Ile Leu Gly Ile Leu Ala Glu Val Leu Ser Ala Val Phe Cys
275                280                285
Glu Val Met Asn Gly Lys Pro Glu Tyr Thr Asp His Leu Thr His Lys
290                295                300
Leu Lys His His Pro Gly Gln Ile Glu Ala Ala Ile Met Glu His
305                310                315                320
Ile Leu Glu Gly Ser Ser Tyr Met Met Leu Ala Lys Lys Leu Gly Glu
                325                330                335
Leu Asp Pro Leu Met Lys Pro Lys Gln Asp Arg Tyr Ala Leu Arg Thr
                340                345                350
Ser Pro Gln Trp Leu Gly Pro Gln Ile Glu Val Ile Arg Ala Ala Thr
                355                360                365
Lys Ser Ile Glu Arg Glu Ile Asn Ser Val Asn Asp Asn Pro Leu Ile
370                375                380
Asp Val Ser Arg Gly Lys Ala Ile His Gly Gly Asn Phe Gln Gly Thr
385                390                395                400
Pro Ile Gly Val Ser Met Asp Asn Thr Arg Leu Ala Ile Ala Ala Ile
                405                410                415
Gly Lys Leu Met Phe Ala Gln Phe Ser Glu Leu Val Asn Asp Phe Tyr
                420                425                430
Asn Asn Gly Leu Pro Ser Asn Leu Ser Gly Gly Arg Asn Pro Ser Leu
                435                440                445
Asp Tyr Gly Phe Lys Gly Ala Glu Ile Ala Met Ala Ser Tyr Cys Ser
450                455                460
Glu Leu Gln Phe Leu Gly Asn Pro Val Thr Asn His Val Gln Ser Ala
465                470                475                480
Glu Gln His Asn Gln Asp Val Asn Ser Leu Gly Leu Ile Ser Ser Arg
                485                490                495
Lys Thr Ala Glu Ala Ile Asp Ile Leu Lys Leu Met Ser Ser Thr Phe
                500                505                510
Met Val Ala Leu Cys Gln Ala Ile Asp Leu Arg His Ile Glu Glu Asn
                515                520                525
Val Lys Asn Ala Val Lys Asn Cys Val Lys Thr Val Ala Arg Lys Thr
530                535                540
Leu Ser Thr Asn Asp Ser Gly His Leu His Asn Ala Arg Phe Cys Glu
545                550                555                560
Lys Asp Leu Leu Leu Thr Ile Asp Arg Glu Ala Val Phe Ala Tyr Ala
                565                570                575
Asp Asp Pro Cys Ser Ala Asn Tyr Pro Leu Met Gln Lys Met Arg Ala
                580                585                590
Val Leu Val Glu His Ala Leu Ala Asn Gly Glu Ala Glu Gln Asp Val
                595                600                605
Gln Thr Ser Val Phe Ala Lys Leu Ala Thr Phe Glu Gln Glu Leu Arg
610                615                620
Ala Val Leu Pro Lys Glu Val Glu Ser Ala Arg Cys Ser Val Glu Asn
625                630                635                640
Gly Thr Ala Ala Gln Gln Asn Arg Ile Ser Glu Cys Arg Ser Tyr Pro
                645                650                655
Leu Tyr Arg Phe Val Arg Lys Glu Leu Gly Thr Glu Tyr Leu Thr Gly
                660                665                670
Glu Lys Thr Arg Ser Pro Gly Glu Glu Val Asp Lys Val Phe Val Ala
                675                680                685
Met Asn Gln Gly Lys His Ile Asp Ala Leu Leu Glu Cys Leu Lys Glu
690                695                700
Trp Asn Gly Glu Pro Leu Pro Ile Cys
705                710

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<210> 110
 <211> 323
 <212> PRT
 <213> Festuca arundinacea

<400> 110
 Met Ala Phe Ser Gly Ser Val Ser Gly Val Val Leu Val Val Ala Ile
 1 5 10 15
 Leu Leu Leu Gly Leu Ala Ala Ala Ser Ala Gln Leu Ser Ala Thr
 20 25 30
 Phe Tyr Asp Ala Ser Cys Pro Ser Ala Leu Ala Thr Ile Lys Ser Ala
 35 40 45
 Val Thr Ala Ala Val Asn Asn Glu Ala Arg Met Gly Ala Ser Leu Leu
 50 55 60
 Arg Leu His Phe His Asp Cys Phe Val Gln Gly Cys Asp Ala Ser Val
 65 70 75 80
 Leu Leu Asn Asp Thr Ala Asn Phe Thr Gly Glu Gln Thr Ala Phe Pro
 85 90 95
 Asn Arg Asn Ser Ile Arg Gly Leu Asn Val Ile Asp Asn Val Lys Ala
 100 105 110
 Gln Val Glu Ala Val Cys Thr Gln Thr Val Ser Cys Ala Asp Ile Leu
 115 120 125
 Ala Val Ala Ala Arg Asp Ser Ile Val Ala Leu Gly Gly Pro Ser Tyr
 130 135 140
 Thr Val Pro Leu Gly Arg Arg Asp Ser Thr Thr Ala Ser Leu Ser Glu
 145 150 155 160
 Ala Asn Arg Asp Leu Pro Pro Pro Ser Ser Asp Leu Ala Asp Leu Val
 165 170 175
 Gly Asn Phe Ser Arg Lys Gly Leu Ser Val Thr Asp Met Val Ala Leu
 180 185 190
 Ser Gly Ala His Thr Ile Gly Arg Ala Ala Cys Leu Asn Phe Arg Ser
 195 200 205
 Arg Ile Tyr Gly Glu Ser Asn Ile Ala Pro Ala Tyr Ala Ala Ser Leu
 210 215 220
 Gln Ala Asn Cys Pro Gln Ser Ala Pro Asn Gly Asp Gly Thr Leu Ala
 225 230 235 240
 Pro Leu Asp Val Ser Thr Pro Asp Ala Phe Asp Asn Ala Tyr Tyr Gly
 245 250 255
 Asn Leu Leu Ser Gln Gln Gly Leu Leu His Ser Asp Gln Gln Leu Phe
 260 265 270
 Asn Gly Gly Ser Thr Asp Ser Leu Val Ser Thr Tyr Ala Ser Asn Ala
 275 280 285
 Ala Gln Phe Ser Gly Asp Phe Ala Ala Ala Met Val Asn Met Gly Asn
 290 295 300
 Ile Gly Val Leu Thr Gly Ala Gln Gly Glu Ile Arg Leu Asn Cys Gly
 305 310 315 320
 Lys Val Asn

<210> 111
 <211> 344
 <212> PRT
 <213> Lolium perenne

<400> 111
 Met Ala Ser Ser Ser Pro Phe Ser Arg Val Ser Gln Leu Ala Val
 1 5 10 15
 Lys Ala Thr Val Leu Ala Ala Val Cys Leu Leu Leu His Gly Gly Gly
 20 25 30
 Gly Ser Ser Ala Ser Ala Ala Glu Leu Cys Val Ser Tyr Asp His
 35 40 45
 Thr Cys Pro Asp Ala Tyr Lys Ile Val Gln Gly Val Leu Val Glu Ala
 50 55 60
 His Lys Ser Asp Pro Arg Ile Phe Ala Ser Leu Ile Arg Leu His Phe
 65 70 75 80

His Asp Cys Phe Val Leu Gly Cys Asp Gly Ser Leu Leu Leu Asp Thr
 85 90 95
 Phe Pro Gly Phe Gln Ser Glu Lys Asp Ala Arg Pro Asn Asn Asn Ser
 100 105 110
 Ala Arg Gly Tyr Pro Val Val Asp Ala Ala Lys Ala Ala Leu Glu Lys
 115 120 125
 Ala Cys Pro Gly Val Val Ser Cys Ala Asp Ile Leu Ala Leu Ala Ala
 130 135 140
 Glu Ile Ser Val Gln Leu Ser Gly Gly Pro Gly Trp Gly Val Leu Leu
 145 150 155 160
 Gly Arg Leu Asp Gly Lys Thr Ser Ser Ile Ala Gly Ala Gln Asn Leu
 165 170 175
 Pro Gly Pro Phe Asp Gly Leu Lys Asn Leu Thr Leu Lys Phe Gln Ala
 180 185 190
 Val Asn Leu Asp Val Thr Asp Leu Val Ala Leu Ser Gly Ala His Thr
 195 200 205
 Phe Gly Arg Val Lys Cys Arg Phe Val Thr Asn Arg Leu Tyr Asn Phe
 210 215 220
 Ser Gly Thr Asn Gln Pro Asp Pro Thr Leu Asn Ala Ala Tyr Arg Ala
 225 230 235 240
 Phe Leu Ser Thr Arg Cys Pro Arg Asn Gly Asp Ala Asn Ser Leu Asn
 245 250 255
 Asp Leu Asp Pro Thr Thr Pro Asp Thr Phe Asp Lys Asn Tyr Phe Thr
 260 265 270
 Asn Leu Glu Lys Asn Arg Gly Phe Leu Asp Ser Asp Gln Gln Leu Lys
 275 280 285
 Ser Asp Pro Gly Ala Leu Thr Thr Ala Pro Ile Val Asp Arg Phe
 290 295 300
 Ala Ser Ser Gln Asp Ala Phe Phe Lys Ser Phe Ala Trp Ser Met Ile
 305 310 315 320
 Lys Met Gly Asn Ile Leu Pro Ile Thr Asp Pro Ser Arg Gly Glu Val
 325 330 335
 Arg Lys His Cys Ala Phe Val Asn
 340

<210> 112

<211> 326

<212> PRT

<213> Festuca arundinacea

<400> 112

Met Ala Thr Arg Gly Val Met Val Ala Leu Leu Leu Ala Ala Val Ala
 1 5 10 15
 Ala Ser Cys Ala His Ala Gln Leu His Glu Lys Phe Tyr Ser Glu Ser
 20 25 30
 Cys Pro Ser Val Glu Asp Val Val Arg Lys Glu Met Val Met Ala Leu
 35 40 45
 Ser Leu Ala Pro Ser Leu Ala Ala Pro Leu Leu Arg Met His Phe His
 50 55 60
 Asp Cys Phe Val Arg Gly Cys Asp Gly Ser Val Leu Leu Asp Ser Ala
 65 70 75 80
 Asn Lys Thr Ala Glu Lys Asp Ala Leu Pro Asn Gln Thr Leu Arg Gly
 85 90 95
 Phe Asp Phe Val Glu Arg Val Lys Ala Ala Val Glu Lys Ala Cys Pro
 100 105 110
 Asp Thr Val Ser Cys Ala Asp Val Val Thr Leu Ile Ala Arg Asp Ala
 115 120 125
 Val Trp Leu Ser Lys Gly Pro Phe Trp Glu Val Pro Leu Gly Arg Arg
 130 135 140
 Asp Gly Ser Val Ser Ile Ser Asn Glu Thr Asp Ala Leu Pro Pro Pro
 145 150 155 160
 Thr Ala Asn Ile Thr Val Leu Thr Gln Leu Phe Ala Ala Lys Asn Leu
 165 170 175
 Asp Ile Lys Asp Leu Val Val Leu Ser Ala Ala His Thr Ile Gly Thr
 180 185 190

Ser His Cys Phe Ser Phe Ser Asp Arg Leu Tyr Asn Phe Thr Gly Leu
 195 200 205
 Asp Asn Ala Ser Asp Ile Asp Pro Thr Leu Glu Pro Phe Tyr Met Ala
 210 215 220
 Lys Leu Lys Ser Lys Cys Thr Ser Leu Asp Asp Asn Ser Thr Leu Val
 225 230 235 240
 Glu Met Asp Pro Gly Ser Phe Lys Thr Phe Asp Leu Asp Tyr Phe Lys
 245 250 255
 Leu Val Ser Lys Arg Arg Gly Leu Phe His Ser Asp Gly Ala Leu Leu
 260 265 270
 Thr Asp Ala Phe Thr Arg Ala Tyr Ile Leu Arg His Ala Thr Gly Ala
 275 280 285
 Phe Lys Asp Glu Phe Phe Ala Asp Phe Ala Val Ser Met Val Lys Met
 290 295 300
 Gly Asn Thr Asp Val Leu Thr Gly Ser Gln Gly Glu Ile Arg Lys Lys
 305 310 315 320
 Cys Ser Val Val Asn His
 325

<210> 113

<211> 358

<212> PRT

<213> Lolium perenne

<400> 113

Met Ala Ser Ser Arg Val Leu Leu Leu Val Val Ala Ala Leu Ala Ile
 1 5 10 15
 Ser Val Ser Ala Thr Ala Ala Ala Thr Lys Ile Ser Ala Pro Leu Pro
 20 25 30
 Pro Leu Ala Lys Gly Leu Asn Phe Asp Phe Tyr Lys Ala Thr Cys Pro
 35 40 45
 Gln Ala Glu Ser Ile Val Phe Asn Phe Leu Arg Asp Ala Ile Arg Lys
 50 55 60
 Asp Val Gly Leu Ala Ala Ala Leu Leu Arg Ile His Phe His Asp Cys
 65 70 75 80
 Phe Val Gln Gly Cys Asp Gly Ser Val Leu Asp Lys Thr Gly Gly
 85 90 95
 Thr Asp Ser Glu Lys Ile Ala Pro Pro Asn Val Thr Leu Arg Pro Thr
 100 105 110
 Ala Phe Lys Ala Ile Asn Asp Leu Arg Ala Leu Leu Ala Lys Ala Cys
 115 120 125
 Gly Ala Val Val Ser Cys Ala Asp Ile Ala Ala Leu Ala Ala Arg Asp
 130 135 140
 Ser Val His Leu Ala Gly Gly Pro His Tyr Pro Val Pro Leu Gly Arg
 145 150 155 160
 Arg Asp Gly Leu Ala Pro Ala Asn Leu Thr Thr Ile Leu Asn Ala Leu
 165 170 175
 Pro Ala Pro Ser Ser Asn Val Thr Thr Leu Leu Arg Phe Leu Ala Lys
 180 185 190
 Ile Ser Leu Asp Ala Asn Asp Leu Val Ala Leu Ser Gly Ala His Thr
 195 200 205
 Leu Gly Ile Ala His Cys Thr Ser Phe Gln Glu Arg Leu Phe Pro Gln
 210 215 220
 Asn Asp Val Thr Leu Asn Lys Trp Phe Ala Ser Gln Leu Arg Leu Thr
 225 230 235 240
 Cys Pro Ala Leu Asn Thr Asp Asn Thr Thr Asn Asn Asp Ile Arg Thr
 245 250 255
 Pro Asn Val Phe Asp Asn Lys Tyr Tyr Val Asp Leu Leu Asn Arg Gln
 260 265 270
 Gly Leu Phe Thr Ser Asp Gln Asp Leu His Thr Asp Ala Arg Thr Lys
 275 280 285
 Pro Thr Val Thr Arg Phe Ala Val Asp Gln Ala Ala Phe Phe Asp Gln
 290 295 300
 Phe Val Phe Ser Val Val Lys Met Gly Gln Ile Asn Val Leu Thr Gly
 305 310 315 320

Ser Gln Gly Gln Ile Arg Asn Asp Cys Ser Ala Pro Asn Lys Gly Arg
 325 330 335
 Thr Asn Asp Asp Leu Pro Trp Ser Val Leu Glu Thr Val Thr Glu Ala
 340 345 350
 Ala Gln Ser Leu Val Leu
 355

<210> 114

<211> 344

<212> PRT

<213> Lolium perenne

<400> 114

Met Thr Thr Met Gly Gly Ser Ser Ile Leu Pro Ala Pro Thr Val Ala
 1 5 10 15
 Thr Thr Ala Leu Val Leu Leu Ile Val Leu Phe Ala Ser Pro Ala Thr
 20 25 30
 Val Ala Lys Gly Ser Gly Leu Ser Val Gly Phe Tyr Lys Lys Leu Cys
 35 40 45
 Pro Lys Ala Glu Lys Val Val Arg Arg Thr Val Thr Lys Ala Phe Glu
 50 55 60
 Lys Glu Pro Gly Thr Pro Ala Asp Ile Ile Arg Leu Phe Phe His Asp
 65 70 75 80
 Cys Phe Val Arg Gly Cys Asp Ala Ser Val Leu Leu Glu Ser Thr Pro
 85 90 95
 Gly Arg Met Ala Glu Arg Asp Ser Lys Ala Asn Asn Pro Ser Leu Asp
 100 105 110
 Gly Phe Glu Val Ile Ser Asp Ala Lys Glu Thr Leu Glu Lys Leu Cys
 115 120 125
 Pro Gln Thr Val Ser Cys Ala Asp Ile Leu Ala Leu Ala Ala Arg Asp
 130 135 140
 Gly Ala Tyr Leu Ala Ser Gly Leu Asp Tyr Ala Val Pro Thr Gly Arg
 145 150 155 160
 Arg Asp Gly Leu Val Ser Lys Glu Asp Glu Val Leu Pro Ser Val Pro
 165 170 175
 His Pro Asp Phe Asn His Ser Gln Leu Val Glu Asn Phe Thr Ala Lys
 180 185 190
 Gly Phe Thr Ala Glu Glu Met Val Thr Leu Ser Gly Ala His Thr Ile
 195 200 205
 Gly Thr Ser His Cys Ser Ser Phe Thr Asp Arg Leu Tyr Asn Phe Ser
 210 215 220
 Gln Gly Gly Ala Leu Thr Thr Asp Pro Ala Leu Pro Ala Ala Tyr Ala
 225 230 235 240
 Ala Leu Leu Lys Glu Lys Cys Pro Pro Glu Thr Ala Ala Gln Asn Asp
 245 250 255
 Thr Thr Met Val Gln Leu Asp Asp Val Thr Pro Phe Val Met Asp Asn
 260 265 270
 Gln Tyr Tyr Lys Asn Leu Leu Ala Gly Thr Val Pro Leu Gly Ser Asp
 275 280 285
 Val Ala Leu Met Glu Ser Pro Asp Thr Ala Ala Leu Val Glu Leu Tyr
 290 295 300
 Ala Arg Glu Pro Ala Glu Tyr Trp Ala Lys Arg Phe Val Ala Ala Met
 305 310 315 320
 Val Lys Val Ser Glu Met Glu Val Leu Thr Gly Ala Glu Gly Glu Ile
 325 330 335
 Arg Leu Asn Cys Ser Lys Val Asn
 340

<210> 115

<211> 293

<212> PRT

<213> Lolium perenne

<400> 115

Thr Arg Glu Asn Tyr Tyr Gly Ser Ser Cys Pro Thr Ala Leu Leu Thr
 1 5 10 15

Ile Arg Thr Val Val Thr Thr Ala Val Leu Leu Asp His Arg Met Gly
 20 25 30
 Ala Ser Leu Leu Arg Leu His Phe His Asp Cys Phe Val Gln Gly Cys
 35 40 45
 Asp Ala Ser Val Leu Leu Asp Asp Thr Ala Gly Phe Thr Gly Glu Lys
 50 55 60
 Gly Ala Gly Pro Asn Ala Gly Ser Leu Arg Gly Leu Glu Val Ile Asp
 65 70 75 80
 Lys Ile Lys Met Leu Leu Glu Phe Met Cys Pro Arg Thr Val Ser Cys
 85 90 95
 Ala Asp Ile Leu Ala Val Ala Ala Arg Asp Ser Val Val Arg Leu Gly
 100 105 110
 Gly Pro Ser Trp Ala Val Gln Leu Gly Arg Arg Asp Ala Thr Thr Ala
 115 120 125
 Ser Ala Ser Leu Ala Ser Ser Asp Leu Pro Gly Pro Asn Ser Asn Leu
 130 135 140
 Asn Asp Leu Leu Thr Ala Phe Ser Lys Lys Gly Leu Ser Thr Thr Asp
 145 150 155 160
 Met Val Ala Leu Ser Gly Ala His Thr Ile Gly Arg Ala Gln Cys Gln
 165 170 175
 Asn Tyr Arg Asn Arg Ile Tyr Thr Asp Thr Asp Ile Asp Gly Ala Phe
 180 185 190
 Ala Ala Ser Leu Arg Gly Gly Cys Pro Gln Ala Gly Gly Asp Gly Asn
 195 200 205
 Leu Ala Pro Leu Asp Ala Ser Ser Pro Asn Thr Phe Asp Asn Gly Tyr
 210 215 220
 Phe Ser Gly Leu Leu Ser Arg Gln Gly Leu Leu His Ser Asp Gln Ala
 225 230 235 240
 Leu Tyr Asp Gly Gly Ser Thr Asp Asp Leu Val Arg Thr Tyr Ala Ser
 245 250 255
 Asn Asn Asp Gln Phe Gly Ser Asp Phe Ala Ala Ala Met Val Lys Leu
 260 265 270
 Ser Asn Ile Gly Leu Leu Thr Gly Ser Ser Gly Glu Ile Arg Val Asn
 275 280 285
 Cys Arg Ala Val Asn
 290

<210> 116

<211> 311

<212> PRT

<213> Festuca arundinacea

<400> 116

Met Ala Ser Ala Ser Cys Ile Ser Leu Val Leu Leu Val Ala Leu Ala
 1 5 10 15
 Ala Thr Ala Ala Ser Ala Gln Leu Ser Ser Thr Phe Tyr Asp Thr Ser
 20 25 30
 Cys Pro Arg Ala Leu Ala Thr Ile Lys Ser Gly Val Ala Ala Ala Val
 35 40 45
 Ser Ser Asn Pro Arg Met Gly Ala Ser Leu Leu Arg Leu His Phe His
 50 55 60
 Asp Cys Phe Val Asn Gly Cys Asp Ala Ser Val Leu Leu Ser Gly Asn
 65 70 75 80
 Glu Gln Asn Ala Pro Ala Asn Ala Gly Ser Leu Phe Gly Phe Gly Val
 85 90 95
 Ile Asp Asn Ile Lys Thr Gln Leu Glu Gly Ile Cys Lys Gln Thr Val
 100 105 110
 Ser Cys Ala Asp Ile Leu Thr Val Ala Ala Arg Asp Ser Val Val Ala
 115 120 125
 Leu Gly Gly Pro Ser Trp Thr Val Pro Leu Gly Arg Arg Asp Ser Thr
 130 135 140
 Ser Ala Thr Gly Asn Thr Gly Asp Leu Pro Gly Pro Gly Ser Ser Leu
 145 150 155 160
 Ala Gln Leu Gln Ala Ala Phe Ala Lys Lys Asn Leu Asn Thr Val Asp
 165 170 175

Met Val Ala Leu Ser Gly Ala His Thr Ile Gly Arg Ala Gln Cys Gln
 180 185 190
 Asn Phe Arg Ser Arg Ile Tyr Gly Gly Asp Ser Asn Ile Asn Ala Ala
 195 200 205
 Phe Ala Thr Ser Leu Lys Ala Asn Cys Pro Gln Ser Gly Gly Asn Gly
 210 215 220
 Asn Leu Ala Ala Leu Asp Ala Thr Thr Ala Asn Ala Phe Asp Asn Ala
 225 230 235 240
 Tyr Tyr Thr Asn Leu Leu Ser Gln Lys Gly Leu Leu His Ser Asp Gln
 245 250 255
 Val Leu Phe Asn Asn Gly Ser Thr Asp Asn Thr Val Arg Asn Phe Ala
 260 265 270
 Ser Ser Gly Ala Ala Phe Ser Ser Ala Phe Ala Thr Ala Met Ile Lys
 275 280 285
 Met Gly Asn Ile Ser Pro Leu Thr Gly Thr Gln Gly Gln Ile Arg Leu
 290 295 300
 Ser Cys Ser Lys Val Asn Ser
 305 310

<210> 117

<211> 230

<212> PRT

<213> Lolium perenne

<400> 117

Met Ala Val Ser Glu Leu Glu Val Asp Gly Val Val Phe Pro Pro Leu
 1 5 10 15
 Ala Arg Pro Pro Gly Thr Ala His Ala His Phe Leu Ala Gly Ala Gly
 20 25 30
 Val Arg Gly Met Glu Leu Gly Gly Asn Phe Ile Lys Phe Thr Ala Ile
 35 40 45
 Gly Val Tyr Leu Gln Ala Asp Ala Ala Val Ser Ala Leu Ala Thr Lys
 50 55 60
 Trp Ala Gly Lys Pro Ala Asp Glu Leu Ala Ala Asp Asn Ala Phe Phe
 65 70 75 80
 Arg Asp Val Val Thr Gly Glu Phe Glu Lys Phe Thr Pro Val Thr Met
 85 90 95
 Ile Leu Pro Leu Thr Gly Ala Gln Tyr Ser Glu Lys Val Thr Glu Asn
 100 105 110
 Cys Val Ala Tyr Trp Lys Ala Val Gly Lys Tyr Thr Asn Ala Glu Ala
 115 120 125
 Ala Ala Val Asp Lys Phe Lys Glu Ala Phe Arg Thr Glu Ser Phe Pro
 130 135 140
 Pro Gly Ala Ser Ile Leu Phe Thr His Ser Pro Ala Gly Val Leu Thr
 145 150 155 160
 Val Ala Phe Ser Lys Asp Ser Ser Val Pro Glu Ser Gly Gly Val Ala
 165 170 175
 Ile Glu Asn Arg Pro Leu Cys Glu Ala Val Leu Glu Ser Ile Ile Gly
 180 185 190
 Glu His Gly Val Ser Pro Ala Ala Lys Leu Ser Leu Ala Thr Arg Val
 195 200 205
 Ala Glu Leu Leu Asn Glu Ala Ala Pro Val Gly Gln Ala Ala Ala Glu
 210 215 220
 Pro Val Ser Val Ser Ala
 225 230

<210> 118

<211> 231

<212> PRT

<213> Festuca arundinacea

<400> 118

Met Ala Val Ser Glu Leu Glu Val Asp Gly Val Val Phe Pro Pro Leu
 1 5 10 15
 Ala Arg Pro Pro Gly Thr Ala His Ala His Phe Leu Ala Gly Ala Gly
 20 25 30

```

Val Arg Gly Met Glu Leu Gly Gly Asn Phe Ile Lys Phe Thr Ala Ile
      35      40      45
Gly Val Tyr Leu Gln Ala Asp Ala Ala Val Ser Ala Leu Ala Ala Lys
      50      55      60
Trp Ala Gly Lys Pro Ala Asp Glu Leu Ala Ala Asp Asn Ala Phe Phe
      65      70      75      80
Arg Asp Val Val Thr Gly Glu Phe Glu Lys Phe Arg Arg Val Thr Met
      85      90      95
Ile Leu Pro Leu Thr Gly Ala Gln Tyr Ser Glu Lys Val Thr Glu Asn
      100      105      110
Cys Val Ala Tyr Trp Lys Ala Val Gly Lys Tyr Thr Asp Ala Glu Ala
      115      120      125
Ala Ala Val Asp Lys Phe Lys Glu Ala Phe Lys Ala Glu Ser Phe Pro
      130      135      140
Pro Gly Ala Ser Ile Leu Phe Thr His Ser Pro Ala Gly Val Leu Thr
      145      150      155      160
Val Ala Phe Ser Lys Asp Ser Ser Leu Pro Glu Ser Gly Gly Val Ala
      165      170      175
Ile Glu Asn Arg Pro Leu Cys Glu Ala Val Leu Lys Ser Ile Ile Gly
      180      185      190
Lys His Gly Val Ser Pro Ala Ala Lys Leu Ser Leu Ala Thr Arg Val
      195      200      205
Ala Glu Leu Leu Lys Glu Ala Ala Pro Val Gly Glu Pro Ala Val Ala
      210      215      220
Glu Pro Val Ser Val Ser Ala
      225      230

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<210> 119

<211> 394

<212> PRT

<213> Lolium perenne

<400> 119

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Met Ala Ala Thr Met Thr Val Glu Glu Val Arg Lys Ala Gln Arg Ala
      1      5      10      15
Glu Gly Pro Ala Thr Val Leu Ala Ile Gly Thr Ala Thr Pro Ala Asn
      20      25      30
Cys Val Tyr Gln Ala Asp Tyr Pro Asp Tyr Tyr Phe Lys Ile Thr Lys
      35      40      45
Ser Asp His Leu Ala Asp Leu Lys Glu Lys Phe Lys Arg Met Cys Asp
      50      55      60
Lys Ser Gln Ile Arg Lys Arg Tyr Met His Leu Thr Glu Glu Ile Leu
      65      70      75      80
Glu Glu Asn Pro Asn Met Cys Ala Tyr Met Ala Pro Ser Leu Asp Ala
      85      90      95
Arg Gln Asp Ile Val Val Val Glu Val Pro Lys Leu Gly Lys Ala Ala
      100      105      110
Ala Gln Lys Ala Ile Lys Glu Trp Gly Gln Pro Arg Ser Lys Ile Thr
      115      120      125
His Leu Val Phe Cys Thr Thr Ser Gly Val Asp Met Pro Gly Ala Asp
      130      135      140
Tyr Gln Leu Thr Lys Met Leu Gly Leu Arg Pro Ser Val Lys Arg Leu
      145      150      155      160
Met Met Tyr Gln Gln Gly Cys Phe Ala Gly Gly Thr Val Leu Arg Leu
      165      170      175
Ala Lys Asp Leu Ala Glu Asn Asn Arg Gly Ala Arg Val Leu Val Val
      180      185      190
Cys Ser Glu Ile Thr Ala Val Thr Phe Arg Gly Pro His Glu Ser His
      195      200      205
Leu Asp Ser Leu Val Gly Gln Ala Leu Phe Gly Asp Gly Ala Ala Ala
      210      215      220
Val Ile Ile Gly Ala Asp Pro Asp Val Ser Val Glu Arg Pro Leu Phe
      225      230      235      240
Gln Leu Val Ser Ala Ser Gln Thr Ile Leu Pro Asp Ser Glu Gly Ala
      245      250      255

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Ile Asp Gly His Leu Arg Glu Val Gly Leu Thr Phe His Leu Leu Lys
 260 265 270
 Asp Val Pro Gly Leu Ile Ser Lys Asn Ile Glu Arg Ala Leu Glu Glu
 275 280 285
 Ala Phe Lys Pro Leu Gly Ile Asp Asp Trp Asn Ser Val Phe Trp Val
 290 295 300
 Ala His Pro Gly Gly Pro Ala Ile Leu Asp Met Val Glu Ala Lys Val
 305 310 315 320
 Asn Leu Asn Lys Glu Arg Met Arg Ala Thr Arg His Val Leu Ser Glu
 325 330 335
 Tyr Gly Asn Met Ser Ser Ala Cys Val Leu Phe Ile Met Asp Glu Met
 340 345 350
 Arg Lys Arg Ser Ala Glu Asp Gly His Thr Thr Thr Gly Glu Gly Met
 355 360 365
 Asp Trp Gly Val Leu Phe Gly Phe Gly Pro Gly Leu Thr Val Glu Thr
 370 375 380
 Val Val Leu His Ser Met Pro Ile Ala Ala
 385 390

<210> 120

<211> 196

<212> PRT

<213> Festuca arundinacea

<400> 120

Met Tyr Phe Val Ser Lys Ser Leu Ala Glu Asn Ala Ala Met Asp Tyr
 1 5 10 15
 Ala Lys Glu Asn Gly Val Asp Phe Ile Ser Ile Ile Pro Thr Leu Val
 20 25 30
 Val Gly Pro Phe Leu Ser Ala Gly Met Pro Pro Ser Leu Val Thr Ala
 35 40 45
 Leu Ala Leu Ile Thr Gly Asn Glu Ala His Tyr Ser Ile Leu Lys Gln
 50 55 60
 Val Gln Leu Val His Leu Asp Asp Leu Cys Asp Ser Met Thr Tyr Leu
 65 70 75 80
 Phe Glu His Pro Asp Ala Asn Gly Arg Tyr Ile Cys Ser Ser His Asp
 85 90 95
 Thr Thr Ile His Gly Ile Ala Arg Met Leu Lys Glu Arg Phe Pro Glu
 100 105 110
 Tyr Asp Ile Pro Gln Lys Phe Pro Gly Ala Asp Asp Asp Leu Gln Pro
 115 120 125
 Ile His Phe Phe Phe Lys Lys Leu Leu Asp His Gly Phe Arg Phe Arg
 130 135 140
 Tyr Thr Ala Glu Asp Met Phe Asp Ala Ala Val Trp Thr Cys Arg Glu
 145 150 155 160
 Lys Gly Leu Ile Pro Leu Gly Ala Glu Gly Ala Gly Gly Pro Ala Ser
 165 170 175
 Ala Ala Gly Lys Leu Gly Ala Val Leu Val Gly Glu Gly Gln Ala Ile
 180 185 190
 Gly Ala Glu Thr
 195

<210> 121

<211> 329

<212> PRT

<213> Lolium perenne

<400> 121

Met Ala Thr Glu Ala Lys Gly Glu Thr Val Leu Val Thr Gly Ala Ser
 1 5 10 15
 Gly Phe Ile Gly Ser Trp Leu Val Arg Leu Leu Leu Ala Arg Gly Tyr
 20 25 30
 Ser Val His Ala Ala Val Leu Asn Pro Asp Asp Lys Ala Glu Thr Asp
 35 40 45
 His Leu Leu Ala Leu Ala Ala Ala Gly Asp Glu Gly Arg Ile Arg
 50 55 60

```

Phe Phe Arg Cys Asp Leu Leu Asp Gly Ala Ala Met Leu Ala Ala Val
65      70      75      80
Arg Gly Cys Ser Gly Val Phe His Leu Ala Ser Pro Cys Thr Val Asn
      85      90      95
Leu Val Leu Asn Pro Gln Lys Glu Leu Val Val Pro Ala Val Glu Gly
      100      105      110
Thr Leu Asn Val Leu Arg Ala Ala Lys Glu Ala Gly Gly Val Arg Arg
      115      120      125
Val Val Val Thr Ser Ser Val Ser Ala Leu Val Pro Cys Pro Gly Trp
      130      135      140
Pro Ala Gly Glu Val Leu Asp Glu Arg Cys Trp Thr Asp Ile Asp Tyr
145      150      155      160
Cys Asp Lys Asn Gly Val Trp Tyr Pro Ala Ser Lys Ala Leu Ala Glu
      165      170      175
Lys Ala Ala Trp Lys Phe Ala Glu Glu Asn Gly Leu Asp Val Val Thr
      180      185      190
Val Asn Pro Gly Thr Val Leu Gly Glu Met Ile Pro Pro Arg Leu Asn
      195      200      205
Ala Ser Met Ala Met Phe Leu Arg Leu Leu Glu Gly Cys Lys Glu Glu
      210      215      220
Tyr Ala Asp Phe Phe Ile Gly Pro Val His Val Glu Asp Val Ala Leu
225      230      235      240
Ala His Ile Leu Leu Tyr Glu Asn Pro Ser Ala Ser Gly Arg His Leu
      245      250      255
Cys Val Glu Pro Ile Cys His Trp Ser Val Phe Ala Ala Lys Val Ala
      260      265      270
Glu Leu Tyr Pro Asp Tyr Lys Val Pro Lys Phe Pro Glu Asp Thr Gln
      275      280      285
Pro Gly Leu Val Arg Ala Lys Ala Val Pro Lys Lys Leu Met Ala Leu
      290      295      300
Gly Leu Gln Phe Thr Pro Leu Glu Lys Ile Ile Arg Asp Ala Val Glu
305      310      315      320
Ser Leu Lys Ser Arg Gly Cys Ile Ala
      325

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<210> 122

<211> 328

<212> PRT

<213> Lolium perenne

<400> 122

```

Gly Ser Thr Lys Gly Lys Val Cys Val Thr Gly Ala Ser Gly Phe Val
1      5      10      15
Ala Ser Trp Leu Ile Lys Lys Leu Leu Glu Ser Gly Tyr His Val Ile
      20      25      30
Gly Thr Val Arg Asp Pro Gly Asn Arg Arg Lys Val Gly His Leu Trp
      35      40      45
Lys Leu Pro Gly Ala Asn Glu Arg Leu Gln Leu Val Arg Ala Asp Leu
      50      55      60
Leu Glu Glu Gly Ser Phe Asp Asp Ala Val Arg Ala Cys Glu Gly Val
65      70      75      80
Phe His Ile Ala Ser Pro Val Leu Gly Lys Ser Asp Ser Asn Cys Lys
      85      90      95
Glu Ala Thr Leu Gly Pro Ala Ile Asn Gly Thr Leu Asn Val Leu Arg
      100      105      110
Ser Cys Lys Lys Ser Pro Phe Leu Lys Arg Val Val Leu Thr Ser Ser
      115      120      125
Ser Ser Ala Val Arg Ile Arg Asp Glu Thr Gln Gln Pro Glu Leu Leu
      130      135      140
Trp Asp Glu Thr Thr Trp Ser Ser Val Pro Leu Cys Glu Lys Leu Gln
145      150      155      160
Leu Trp Tyr Ala Leu Ala Lys Val Phe Ala Glu Lys Ala Ala Leu Asp
      165      170      175
Phe Ala Lys Glu Asn Asn Ile Asp Leu Val Thr Val Leu Pro Ser Phe
      180      185      190

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Val Ile Gly Pro Ser Leu Ser His Glu Leu Cys Thr Thr Ala Ser Asp
    195          200          205
Ile Leu Gly Leu Leu Gln Gly Asp Thr Asp Arg Phe Thr Leu Tyr Gly
    210          215          220
Arg Met Gly Tyr Val His Ile Asp Asp Val Ala Arg Ser His Ile Leu
    225          230          235          240
Val Tyr Glu Thr Pro Glu Ala Thr Gly Arg Tyr Leu Cys Ser Ser Val
    245          250          255
Val Leu Asp Asn Asn Glu Leu Val Gly Leu Leu Ala Lys Gln Phe Pro
    260          265          270
Val Phe Pro Ile Pro Arg Arg Leu Lys Asn Pro Tyr Gly Lys Gln Ala
    275          280          285
Tyr Gln Leu Asp Thr Ser Lys Leu Gln Gly Leu Gly Leu Lys Phe Lys
    290          295          300
Gly Val Gln Glu Met Phe Asn Asp Cys Val Glu Ser Leu Lys Asp Gln
    305          310          315          320
Gly His Leu Leu Glu Cys Pro Leu
    325

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<210> 123

<211> 369

<212> PRT

<213> Lolium perenne

<400> 123

```

Met Ala Pro Val Val Glu Arg Ala Pro Phe Leu Pro Thr Gly Glu Ala
  1          5          10          15
Thr Leu Arg Pro Ser Phe Val Arg Asp Glu Asp Glu Arg Pro Lys Val
    20          25          30
Ala His Asp Arg Phe Ser Asp Glu Val Pro Val Ile Ser Leu His Gly
    35          40          45
Ile Asp Asp Ala Arg Arg Thr Glu Ile Arg Asp Arg Val Ala Ala Ala
    50          55          60
Cys Glu Gly Trp Gly Ile Phe Gln Val Val Asp His Gly Val Asp Ala
    65          70          75          80
Ala Leu Ile Ala Glu Met Ala Arg Leu Ser Arg Asp Phe Phe Ala Leu
    85          90          95
Pro Ala Glu Asp Lys Leu Arg Tyr Asp Met Ser Gly Gly Lys Lys Gly
    100          105          110
Gly Phe Ile Val Ser Ser His Leu Gln Gly Glu Thr Val Gln Asp Trp
    115          120          125
Arg Glu Ile Val Thr Tyr Phe Ser Tyr Pro Val Lys Ala Arg Asp Tyr
    130          135          140
Gly Arg Trp Pro Asp Lys Pro Ala Gly Trp Arg Ala Val Val Glu Gln
    145          150          155          160
Tyr Ser Glu Arg Leu Met Ala Leu Ser Cys Lys Leu Leu Gly Val Leu
    165          170          175
Ser Glu Ala Met Gly Leu Glu Thr Glu Ala Leu Ser Lys Ala Cys Val
    180          185          190
Asp Met Asp Gln Lys Val Val Val Asn Phe Tyr Pro Lys Cys Pro Gln
    195          200          205
Pro Asp Leu Thr Leu Gly Leu Lys Arg His Thr Asp Pro Gly Thr Ile
    210          215          220
Thr Leu Leu Leu Gln Asp Leu Val Gly Gly Leu Gln Ala Thr Arg Asp
    225          230          235          240
Gly Gly Asn Thr Trp Ile Thr Val Gln Pro Ile Ala Gly Ala Phe Val
    245          250          255
Val Asn Leu Gly Asp His Gly His Tyr Leu Ser Asn Gly Arg Phe Lys
    260          265          270
Asn Ala Asp His Gln Ala Val Val Asn Gly Glu Ser Ser Arg Leu Ser
    275          280          285
Ile Ala Thr Phe Gln Asn Pro Ala Pro Asp Ala Lys Val Trp Pro Leu
    290          295          300
Ala Val Arg Glu Gly Glu Asp Thr Ile Leu Glu Glu Pro Ile Thr Phe
    305          310          315          320

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Thr Glu Met Tyr Arg Arg Lys Met Ala Arg Asp Leu Glu Leu Ala Lys
 325 330 335
 Arg Lys Lys Gln Ala Lys Ala Asp Gln Leu Lys Gln Gln Leu Gln Gln
 340 345 350
 Glu Ala Ala Pro Ala Ala Ala Pro Thr Lys Pro Leu Asn Gln Ile Leu
 355 360 365
 Ala

<210> 124

<211> 380

<212> PRT

<213> Festuca arundinacea

<400> 124

Met Ala Ser Val Glu Asn Ala Pro Phe Leu Pro Thr Ala Ala Thr Gly
 1 5 10 15
 Glu Ala Thr Leu Arg Pro Ser Phe Val Arg Asp Glu Asp Glu Arg Pro
 20 25 30
 Lys Val Ala His Asp Arg Phe Ser Asp Glu Val Pro Val Ile Ser Leu
 35 40 45
 His Gly Ile Asp Asp Gly Gly Ala Arg Arg Ala Glu Ile Arg Asp Arg
 50 55 60
 Val Ala Ala Ala Cys Glu Gly Trp Gly Val Phe Gln Val Val Asp His
 65 70 75 80
 Gly Val Asp Ala Ala Leu Val Ala Glu Met Ala Arg Leu Ser Arg Glu
 85 90 95
 Phe Phe Ala Leu Pro Ala Glu Asp Lys Leu Arg Tyr Asp Met Ser Gly
 100 105 110
 Gly Lys Lys Gly Gly Phe Ile Val Ser Ser His Leu Gln Gly Glu Thr
 115 120 125
 Val Gln Asp Trp Arg Glu Ile Val Thr Tyr Phe Ser Tyr Pro Val Lys
 130 135 140
 Ala Arg Asp Tyr Gly Arg Trp Pro Glu Lys Pro Ala Gly Trp Arg Ala
 145 150 155 160
 Val Val Glu Gln Tyr Ser Glu Arg Leu Met Ala Leu Ser Cys Lys Leu
 165 170 175
 Leu Gly Val Leu Ser Glu Ala Met Gly Leu Glu Thr Glu Ala Leu Ser
 180 185 190
 Lys Ala Cys Val Asp Met Asp Gln Lys Val Val Val Asn Phe Tyr Pro
 195 200 205
 Lys Cys Pro Gln Pro Asp Leu Thr Leu Gly Leu Lys Arg His Thr Asp
 210 215 220
 Pro Gly Thr Ile Thr Leu Leu Leu Gln Asp Leu Val Gly Gly Leu Gln
 225 230 235 240
 Ala Thr Arg Asp Gly Gly Asn Thr Trp Ile Thr Val Gln Pro Val Pro
 245 250 255
 Gly Ala Phe Val Val Asn Leu Gly Asp His Gly His Tyr Leu Ser Asn
 260 265 270
 Gly Arg Phe Lys Asn Ala Asp His Gln Ala Val Val Asn Gly Glu Ser
 275 280 285
 Ser Arg Leu Ser Ile Ala Thr Phe Gln Asn Pro Ala Pro Glu Ala Lys
 290 295 300
 Val Trp Pro Leu Ala Val Arg Glu Gly Glu Asp Thr Ile Leu Glu Glu
 305 310 315 320
 Pro Ile Thr Phe Thr Glu Met Tyr Arg Arg Lys Met Ala Cys Asp Leu
 325 330 335
 Glu Leu Ala Lys Arg Lys Lys Gln Ala Lys Ala Asp Gln Leu Lys Gln
 340 345 350
 Gln Leu Gln Gln Glu Gln Gln Glu Ala Val Ala Ala Ala Pro Lys
 355 360 365
 Pro Ala Thr Thr Lys Pro Leu Asn Gln Ile Leu Ala
 370 375 380

<210> 125
 <211> 2105
 <212> DNA
 <213> *Lolium perenne*

<400> 125
 acttagcctt cctcggaaacc atcgaccggg ccgcccggcga cgcgacgcga cgcgatggag 60
 tccagcgccg tcgtccccgg caccacggcg ccgctgcttc cttatgcgta cgcgccgctg 120
 ccgtcgctcct ccgacgacgc ccgtgaaaac agaagtagcg gcggcgtagg gtggcgcgcg 180
 tgcgcgcggc ttctggcggc ctcggcgttg gcggtgggtg tcgtgggtcg gctcctcgcg 240
 ggcggcaggg tggatcgggt ccgcccggc gcagacgtgg cgtcggccac ggtgccggcc 300
 gtgccgatgg agttcccag gagccggggc aaggacttgg gcgtgtcgga gaagtcctcc 360
 ggtgcctact ccgcccagcg cgggttcccg tggagcaacg ccatgctgca gtggcagcgc 420
 accgggttcc atttccagcc ggagcagcac tacatgaacg atcccaacgg ccccggtgtac 480
 tacggcggat ggtaccacct cttctaccag cacaacccca agggcgacag ctggggcaac 540
 atcgcttggg cccacgccgt gtccaaggac atggtcaact ggcgccacct cccgctcgcc 600
 atggttcccg accagtggta cgacagcaac ggcgtcctca ccggtcccat caccgtgctc 660
 cccgacggcc aggtatcct gctctacacc ggcaacaccg acaccctagc ccaggtccag 720
 tgcctcgcca cggccggcga cccgtccgac ccgctcctcc gcgaatggat caagcaccoc 780
 gccaaaccca tcctcttccc gcccccggg atcgggctca aggacttccg cgaccgcctc 840
 accgcctggg tcgaccactc cgaccacacc tggcgccaccg tcatcgggtc caaggacgac 900
 gacggccacg ccggcatcat cctcagctac aagaccaagg acttcgtcaa ctacgagctc 960
 atgcccgga acatgcaccg cgggcccgcac ggcaccggca tgtacgagtg catcgacctc 1020
 taccocgtcg gcggcaactc gtccggagatg ctccggcgcg acgactcgcc cgacgtgctc 1080
 ttctgtctca aggagagcag cgatgacgaa cgtcacgact actatgcgct cggaagggtc 1140
 gacgcgctcg ccaacgtttg gacgcccac gaccgggacc tggaccttgg gatcgggctc 1200
 agatacgact ggggaaagta ctacgcctcc aagtcccttc acgaccagaa gaagaaccgc 1260
 cgcctcgat gggcatacat cggcgagacc gactccgagc aggcgcgacat caccagggga 1320
 tgggccaatc tcatgacgat tccaagaacg gtggagcttg acaggaagac ccgcacaaac 1380
 ctcatccaat ggccagtggg ggaggtcgac accctccgca ggaactccac ggacctcggt 1440
 cgcctcaccg tcaacgccgg ctccgtcatt cgcctccccc tccaccaggg cgctcaactc 1500
 gacatcgagg cctccttcca actcaactct tccgacgtgg atgctatcaa cgaggccgac 1560
 gtccgtctaca cagcgagcac cagcggtgcc cgcagctggg ggcgctcggt ccccttggc 1620
 ctccctcgctc ttgccaatgg ccgcaccgaa cagacggctg tgtacttcta cgtgtccaag 1680
 ggcgtcgacg gcggcctcca gaccacttt tgccacgacg agtcacggtc aacacgggca 1740
 aaggatgtcg tgaataggat gattggcagc atcgtgccgg tgcttgacgg tgagaccttt 1800
 tcggtgaggg tgctagtggg ccaactccatc gtgcagagct tcgcatggg cgaggagatc 1860
 acggcgacgt ccggggcgta cccgacggag gccatctacg cggccgcagg ggtctacctc 1920
 ttcaacaacg ccacgggcgc caccgtcacc gccgagaggc tcgtcgtgca cgagatggcc 1980
 tcagctgaca accatatctt caogaacgac gacttgtaga tgaaaccaag tttagctcgt 2040
 gttgcattct tggttaacggc cgggtgattgc ctatctacac attcatttgg cgttcaaaaa 2100
 aaaaa 2105

<210> 126
 <211> 2068
 <212> DNA
 <213> *Festuca arundinacea*

<400> 126
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<210> 127

<211> 2198

<212> DNA

<213> *Lolium perenne*

<400> 127

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<210> 128
 <211> 2208
 <212> DNA
 <213> *Lolium perenne*

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 <211> 1790
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 <213> *Festuca arundinacea*

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<210> 130

<211> 3633

<212> DNA

<213> Festuca arundinacea

<400> 130

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<210> 131

<211> 3747

<212> DNA

<213> *Lolium perenne*

<400> 131

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<211> 3743

<212> DNA

<213> *Lolium perenne*

<400> 132

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<210> 133

<211> 2714

<212> DNA

<213> Lolium perenne

<400> 133

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<211> 2957

<212> DNA

<213> *Lolium perenne*

<400> 134

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<210> 135

<211> 1986

<212> DNA

<213> Festuca arundinacea

<400> 135

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<210> 136

<211> 2073

<212> DNA

<213> Lolium perenne

<400> 136

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<210> 137

<211> 1888

<212> DNA

<213> Festuca arundinacea

<400> 137

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<210> 138

<211> 1849

<212> DNA

<213> Lolium perenne

<400> 138
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<210> 139

<211> 2166

<212> DNA

<213> *Lolium perenne*

<400> 139
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<210> 140

<211> 2137

<212> DNA

<213> Lolium perenne

<400> 140

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<210> 141

<211> 1954

<212> DNA

<213> Lolium perenne

<400> 141

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<210> 142

<211> 2039

<212> DNA

<213> Lolium perenne

<400> 142

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<210> 143
 <211> 2006
 <212> DNA
 <213> *Lolium perenne*

<400> 143						
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<210> 144
 <211> 1789
 <212> DNA
 <213> *Lolium perenne*

<400> 144						
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<210> 145

<211> 1358

<212> DNA

<213> *Lolium perenne*

<400> 145

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<210> 146

<211> 1051

<212> DNA

<213> *Lolium perenne*

<400> 146

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<210> 147

<211> 1332

<212> DNA

<213> *Lolium perenne*

<400> 147

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<210> 148

<211> 1236

<212> DNA

<213> *Festuca arundinacea*

<400> 148

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<210> 149

<211> 1428

<212> DNA

<213> *Festuca arundinacea*

<400> 149

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<210> 150

<211> 1455

<212> DNA

<213> *Lolium perenne*

<400> 150

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<210> 151

<211> 2101

<212> DNA

<213> *Lolium perenne*

<400> 151
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<210> 152
<211> 2460
<212> DNA
<213> *Lolium perenne*

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<210> 153

<211> 2595

<212> DNA

<213> Festuca arundinacea

<400> 153

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gtcatacccg	ctctatcgct	tcgtgcgcaa	ggactcggg	actgagtatt	tgaccggaga	2160
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gcacattgac	gcgctgcttg	agtgcctcaa	ggagtggaa	ggtgagcccc	tcctatctg	2280
ctgaagaatg	gctcaaggaa	ctcaagaata	gagtgcctga	gaattcagat	ggtactgttt	2340
tataattata	tctccggata	tcgatgtttg	caatgttcc	ccagagctgc	aatgccagtt	2400

agaaaagata	atagcatgac	ttggtagtgt	tgttttagcct	agaaatttttc	tatgatgtta	2460
gttagtaaaa	gggtacactt	tgtgataaat	atacataatt	attgcactag	tcctttattt	2520
ttatatcaat	gttctgtcta	ctgaggcaac	tttgaaggat	tcaaagaatc	tagtattggc	2580
ctgccaacaaa	aaaaa					2595

<210> 154

<211> 1382

<212> DNA

<213> *Lolium perenne*

<400> 154

ggccacaact	cgccacatct	ggcatagcga	gcactgacag	tgagctacat	ccatcaccat	60
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ggccgcgcc	accaagatca	gtgctccact	accgcccgtg	gccaagggcc	tgaacttcca	180
tttctacaag	gccacctgcc	cgcaggccga	gtccatcgtc	ttcaacttcc	tccgcgacgc	240
catccgcaag	gacgtcggcc	togccgccgc	gtccctccgc	atccacttcc	acgactgctt	300
cgtgcagggc	tgcgacggct	ccgtgctcct	cgacaagacc	ggcggcaccg	acagcgagaa	360
gatcgacca	cccaacgtca	cgtccgcccc	caccgccttc	aaggccatca	acgacctccg	420
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cgcgcgcgac	tccgtgcacc	tcgccggcgg	gccgcactac	cccgtcccgc	tcggccgcgc	540
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gtgtcgaatg	acgactagaa	aattgagatg	aatatttgat	gttattttca	ataaaaaaaaa	1380
aa						1382

<210> 155

<211> 1260

<212> DNA

<213> *Lolium perenne*

<400> 155

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ggcgacgacg	gcgctgggtc	tgctgatcgt	gctgttcgca	tcgccggcaa	cgggtggcga	120
aggttctggg	ctgtccgctc	ggttctacaa	gaagtgtgtg	ccgaaggcgg	agaaggctcg	180
ccggcgaaact	gtcaccaagg	cctttgagaa	ggagcctggc	accccgcccg	acatcatccg	240
cctcttcttt	cacgactgct	ttgtccgagg	gtgcgacgca	tcggtgctgc	tggaatccac	300
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cttcacggac	cgcctctaca	acttctccca	ggcgggcgcg	ctgaccacgg	accctgcgct	720
gccggcgcca	tacgccgcgc	tgctgaagga	gaagtgcgcc	ccggagacag	cggcgagaaa	780
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tcatttgggt	tcatatgggtg	gtgagaaata	tatacacatt	tgtttgcgtc	ataaactgta	1200
tagctttacac	agcatgcata	aaagcatcta	tatcattcca	tttgagttgt	aaaaaaaaaa	1260

<210> 156
 <211> 1204
 <212> DNA
 <213> *Lolium perenne*

<400> 156
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 gcggtagcga acgcacagct atcagagaac tactacgggt cttcttgtcc caccgcgtt 180
 ctcaccatca ggactgtcgt gacgacggcg gtgctgtcgt accaccgcat gggcgcttct 240
 cttctccggc tccacttcca cgactgcttt gtgcaagggt gcgacgcgtc cgttctgtctg 300
 gatgacacgg ccggcttcac cggcgagaag ggggccgggc cgaacgcggc gtcgctgctg 360
 ggtctggagg tgatcgacaa gatcaagatg ctgctggagt tcatgtgccc gcggaccgtc 420
 tccctgcggc acatcctcgc cgtcgcggcc cgcgactccg tcgtccgtct aggggggcca 480
 tcatgggchg ttcaacttgg aaggagggac gccaccacag caagcgcgct acttgctagt 540
 agtgacctcc caggcccca ctccaacctc aatgatctcc tcaccgcttt ctccaaaaaa 600
 ggactaagca ccacggacat ggttgcctta tcaggggccc ataccatcgg ccgggchgag 660
 tgccagaact accggaaccg gatctacacc gacaccgaca ttgacggggc attcgacgcg 720
 tccctgcgag gcgctgccc acaggccggc ggcgacggca acctcgcgcc gctcgacgcg 780
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 cgatggatgg atgggggcat catgaaacga acaaggcggt cgatttccgg aactgcaggc 1080
 aacgaaactg catatttatg tacactgcct atttatttcc tgccttctgt tcccctgtct 1140
 gttatattac atccataatc catgttaaga tgggtggcatt ggtttaaaaa aaaaaaaaaa 1200
 aaaa 1204

<210> 157
 <211> 1530
 <212> DNA
 <213> *Lolium perenne*

<400> 157
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 ccgcgacgat gaccgtggag gaggtgagga aggcacagcg ggcggagggg ccggcgacgg 180
 tcttgcccat cggcacggcg acgcccgtta actgtgtcta ccaggctgac taccggact 240
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 tgtgcgacaa gtctcagatc aggaagaggt acatgcacct gacggaggag atcctggagg 360
 agaaccccaa catgtgcgcg tacatggcgc cgtcgttgga cgcgcgccag gacatagttg 420
 tcgtcgaggt cccgaagctc gggaaggcgg cggcacagaa ggcgatcaag gattggggcc 480
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 aaaacaaccg cggcgcgcgc gtgctggtgg tctgctcgga gatcacggcc gtgaccttcc 720
 gcggcccgcga cgagtcacac ctgcactcgc tggctcgcca ggcgctcttc ggggacggcg 780
 ctgcccgggt gataatcggc gccgaccccg acgtgtccgt cgagcgcccg ctgttccagc 840
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 gggaggctcg cctcaccttc cacctcctca aggacgtgcc cgggctcatc tccaagaaca 960
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 tcaacaagga gcggatcggt gccaccaggc acgtcctctc cgagtacggc aacatgtcca 1140
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 aaacggagta cggtttatgt aaaaaaaaaa 1530

<210> 158
 <211> 1418
 <212> DNA
 <213> *Festuca arundinacea*

<400> 158

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tgagcggcaa	caaagggccg	gtggtggtga	ccggggcgtc	gggtttcgtc	gggtcatggc	180
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tcttccacgt	cggcacgccc	atggacttcg	agtccaagga	ccctgagaac	gaagtgatca	420
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agatgtactt	cgtgtccaag	tccctggcgg	agaaggccgc	catggactac	gccaaggaga	660
acggcggtgga	cttcacagc	atcatcccca	cgctcgtcgt	cgcccccttc	ctcagcgccg	720
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cgatcctgaa	gcaggtgcag	ctggtccacc	tggacgacct	ctgcgactcc	atgacctacc	840
tcttcgagca	cccgagcgcc	aacggccgct	acatctgctc	ctcccacgac	accaccattc	900
atggcatcgc	caggatgtct	aaggagaggt	tccccgagta	cgacatccca	cagaaattcc	960
cgggagtcga	cgacgacctc	cagccgatcc	acttcttctt	caagaagctg	ctcgaccacg	1020
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tgcattgtaca	ctaggtctgg	tacctcagac	acatggtgga	gcgatgatta	tgttcgttaa	1260
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tattatgaac	ggattatgga	acgcaaataa	cttcatgaca	aaaaaaaaaa	aaaaaaaaaa	1380
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa			1418

<210> 159

<211> 1209

<212> DNA

<213> *Lolium perenne*

<400> 159

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gcttcatcgg	ctcctggctc	gtccgcctcc	tcctcgccc	cggtactctc	gtccacgccc	120
ccgtcctcaa	ccccgatgac	aaggccgaga	cggaccacct	cctcgcgctc	gccgctgcgg	180
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tgccgcgcgc	caagggaagct	gggggagtg	ggcggttggt	ggtgacctcc	tccgtctccg	420
ccctcgctcc	ctgcccgggg	tggccggccg	gcgaggtcct	cgacgagcgc	tgctggaccg	480
acatcgacta	ctgcgacaag	aacgggggtt	ggtaccctgc	ttcaaaggca	ctggcgaggga	540
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cggtttttgg	cgagatgatt	cgcccaaggc	tcaatgccag	catggccatg	tttcttcgct	660
tacttgaagg	ttgcaaagag	gagtatgcag	atttcttcat	cgggccagtg	cacgtggaag	720
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gcgtggagcc	catctgtcac	tggagtgttt	tcgcccggaa	agtcgcccag	ctctaccctg	840
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atgccgtgga	gagcctcaag	agcagaggat	gcatcgccct	atgattggat	cgtagggcat	1020
gtcacccttc	cgtcgtagg	tcatgatcat	ccttggttag	agatgtgttg	tgttggtgcc	1080
agcccagtg	ctaccagac	catatactta	ccagtatgat	ttgtgcaata	acagccgggt	1140
gatgtacggc	atcacctgcc	ctacacttgg	gatgcggatg	ctgtcacact	gactccctca	1200
aaaaaaaaaa						1209

<210> 160

<211> 1260

<212> DNA

<213> *Lolium perenne*

<400> 160

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tggggcttca	ggctttgttg	cctcttggct	catcaagaaa	ctccttgagt	ctggatatca	120
tgtgataggg	actgtcagag	acccagggaa	tcgaagaaag	gtgggacacc	tttggaact	180
accaggtgca	aatgagaggc	tccaacttgt	gagagctgat	ctattggagg	aagggagctt	240
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gctaagatcc	tgcaagaaga	gtccattttct	caaaagggtt	gttctcacat	cttcatcatc	420
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gagctctgtg	ccactctgtg	aaaagctaca	gctatgggat	gccctggcaa	aggatatttgc	540
agagaaagca	gcattggact	ttgccaagga	gaataacatt	gaccttgtga	cagttcttcc	600
atcattcgta	attggaccca	gtttatccca	tgaattgtgc	actactgctt	cagatatcct	660
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<210> 161

<211> 1438

<212> DNA

<213> Lolium perenne

<400> 161

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ccgtccttcg	tgcgggacga	ggacgagcgg	ccaaggtgg	cgcacgaccg	cttcagcgac	180
gaggtgcccg	tcatctcgct	ccacggcatc	gacgacgcgc	ggaggaccga	gatccgggac	240
cgcgtggcgg	cggcgtgcga	gggggtgggg	atcttccagg	tcgtcgacca	cggcgtcgac	300
gccgcgctca	tcgccgagat	ggccaggctc	tcgcgcgact	tcttcgcgct	ccccgcgag	360
gacaagctcc	gctacgacat	gtccggcggc	aagaagggcg	gattcatcgt	ctccagccac	420
ctccaggcgg	agacggtcca	ggactggcgg	gagatcgtga	cctacttctc	gtaccgggtc	480
aaggcgcggg	actacggccg	gtggccggac	aagcccgcgg	ggtggcgcg	ggtgggtggg	540
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<210> 162

<211> 1214

<212> DNA

<213> Lolium perenne

<400> 162

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gacgtccgtg	gcggtagcga	acgcacagct	atcagagaaac	tactacgggt	cttcttgtcc	180
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agggggggcca	tcttggggcg	ttcaacttgg	aaggagggac	gccaccacag	caagcgcgtc	540
acttgctagt	agtgacctcc	caggccccaa	ctccaacctc	aatgatctcc	tcaccgcttt	600
ctccaaaaaa	ggactaagca	ccacggacat	ggttgctcta	tcaggggccc	ataccatcgg	660
ccgggcgcag	tgcagaaact	accggaaccg	gatctacacc	gacaccgaca	ttgacggggc	720
attcgcagcg	tccctgcgag	gcggtgcgcc	acaggccggc	ggcgacggca	acctcgcgcc	780

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gctcgacgcg tcctctccca acaccttcga taacggctac ttctccggcc tcctctcccg 840
ccaggggctg ctccattccg accaggcgct gtacgacggc ggctccacgg acgatctggg 900
caggacctac gcctccaata acgatcagtt tggcagcgac ttcgctgcgg cgatggtgaa 960
actgagcaat atcggcctgc tgacgggggc gtcgggggag atcagggtca actgccgggc 1020
ggtgaattaa cgatggatgg atgggggcat catgaaacga acaaggcgtg cgatttcggg 1080
aactgcaggc aacgaaactg catatztatg tacactgcct atttatttcc tgccttctgtg 1140
tccccgtctt gttatattac atccataatc catgttaaga tgggtggcatt ggtttaaaaa 1200
aaaaaaaaaaaa 1214

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<210> 163

<211> 654

<212> PRT

<213> *Lolium perenne*

<400> 163

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Met Glu Ser Ser Ala Val Val Pro Gly Thr Thr Ala Pro Leu Leu Pro
1      5      10      15
Tyr Ala Tyr Ala Pro Leu Pro Ser Ser Asp Asp Ala Arg Glu Asn
20     25     30
Arg Ser Ser Gly Gly Val Arg Trp Arg Ala Cys Ala Ala Val Leu Ala
35     40     45
Ala Ser Ala Leu Ala Val Val Val Val Gly Leu Leu Ala Gly Gly
50     55     60
Arg Val Asp Arg Val Pro Ala Gly Ala Asp Val Ala Ser Ala Thr Val
65     70     75     80
Pro Ala Val Pro Met Glu Phe Pro Arg Ser Arg Gly Lys Asp Leu Gly
85     90     95
Val Ser Glu Lys Ser Ser Gly Ala Tyr Ser Ala Asp Gly Gly Phe Pro
100    105    110
Trp Ser Asn Ala Met Leu Gln Trp Gln Arg Thr Gly Phe His Phe Gln
115    120    125
Pro Glu Gln His Tyr Met Asn Asp Pro Asn Gly Pro Val Tyr Tyr Gly
130    135    140
Gly Trp Tyr His Leu Phe Tyr Gln His Asn Pro Lys Gly Asp Ser Trp
145    150    155    160
Gly Asn Ile Ala Trp Ala His Ala Val Ser Lys Asp Met Val Asn Trp
165    170    175
Arg His Leu Pro Leu Ala Met Val Pro Asp Gln Trp Tyr Asp Ser Asn
180    185    190
Gly Val Leu Thr Gly Ser Ile Thr Val Leu Pro Asp Gly Gln Val Ile
195    200    205
Leu Leu Tyr Thr Gly Asn Thr Asp Thr Leu Ala Gln Val Gln Cys Leu
210    215    220
Ala Thr Pro Ala Asp Pro Ser Asp Pro Leu Leu Arg Glu Trp Ile Lys
225    230    235    240
His Pro Ala Asn Pro Ile Leu Phe Pro Pro Gly Ile Gly Leu Lys
245    250    255
Asp Phe Arg Asp Pro Leu Thr Ala Trp Phe Asp His Ser Asp His Thr
260    265    270
Trp Arg Thr Val Ile Gly Ser Lys Asp Asp Asp Gly His Ala Gly Ile
275    280    285
Ile Leu Ser Tyr Lys Thr Lys Asp Phe Val Asn Tyr Glu Leu Met Pro
290    295    300
Gly Asn Met His Arg Gly Pro Asp Gly Thr Gly Met Tyr Glu Cys Ile
305    310    315    320
Asp Leu Tyr Pro Val Gly Gly Asn Ser Ser Glu Met Leu Gly Gly Asp
325    330    335
Asp Ser Pro Asp Val Leu Phe Val Leu Lys Glu Ser Ser Asp Asp Glu
340    345    350
Arg His Asp Tyr Tyr Ala Leu Gly Arg Phe Asp Ala Val Ala Asn Val
355    360    365
Trp Thr Pro Ile Asp Arg Asp Leu Asp Leu Gly Ile Gly Leu Arg Tyr
370    375    380
Asp Trp Gly Lys Tyr Tyr Ala Ser Lys Ser Phe Tyr Asp Gln Lys Lys
385    390    395    400

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Asn Arg Arg Ile Val Trp Ala Tyr Ile Gly Glu Thr Asp Ser Glu Gln
      405      410
Ala Asp Ile Thr Lys Gly Trp Ala Asn Leu Met Thr Ile Pro Arg Thr
      420      425      430
Val Glu Leu Asp Arg Lys Thr Arg Thr Asn Leu Ile Gln Trp Pro Val
      435      440      445
Glu Glu Val Asp Thr Leu Arg Arg Asn Ser Thr Asp Leu Gly Arg Ile
      450      455      460
Thr Val Asn Ala Gly Ser Val Ile Arg Leu Pro Leu His Gln Gly Ala
      465      470      475      480
Gln Leu Asp Ile Glu Ala Ser Phe Gln Leu Asn Ser Ser Asp Val Asp
      485      490      495
Ala Ile Asn Glu Ala Asp Val Gly Tyr Asn Cys Ser Thr Ser Gly Ala
      500      505      510
Ala Val Arg Gly Ala Leu Gly Pro Phe Gly Leu Leu Val Leu Ala Asn
      515      520      525
Gly Arg Thr Glu Gln Thr Ala Val Tyr Phe Tyr Val Ser Lys Gly Val
      530      535      540
Asp Gly Gly Leu Gln Thr His Phe Cys His Asp Glu Ser Arg Ser Thr
      545      550      555      560
Arg Ala Lys Asp Val Val Asn Arg Met Ile Gly Ser Ile Val Pro Val
      565      570      575
Leu Asp Gly Glu Thr Phe Ser Val Arg Val Leu Val Asp His Ser Ile
      580      585      590
Val Gln Ser Phe Ala Met Gly Gly Arg Ile Thr Ala Thr Ser Arg Ala
      595      600      605
Tyr Pro Thr Glu Ala Ile Tyr Ala Ala Ala Gly Val Tyr Leu Phe Asn
      610      615      620
Asn Ala Thr Gly Ala Thr Val Thr Ala Glu Arg Leu Val Val His Glu
      625      630      635      640
Met Ala Ser Ala Asp Asn His Ile Phe Thr Asn Asp Asp Leu
      645      650

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<210> 164

<211> 620

<212> PRT

<213> Festuca arundinacea

<400> 164

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Met Glu Ser Arg Ala Phe Pro Asn Ala Ala Tyr Ala Pro Leu Leu Pro
  1      5      10
Pro Thr Ala Asp Ala Thr Leu Gly Lys Gln Asp Arg Pro Gly Val
  20      25      30
Gly Trp Arg Gly Phe Leu Thr Val Leu Ala Ala Ser Gly Val Val Val
  35      40      45
Leu Leu Val Ala Ala Thr Met Leu Ala Gly Ser Arg Met Gly Gln Ala
  50      55      60
Gly Asp Thr Asp Glu Asp Gly Ala Gly Gly Phe Pro Trp Ser Asn Glu
  65      70      75      80
Met Leu Gln Trp Gln Arg Ala Gly Phe His Tyr Gln Pro Glu Gly His
  85      90      95
Phe Met Ser Asp Pro Asp Gly Pro Val Tyr Tyr Arg Gly Tyr Tyr His
  100      105      110
Leu Phe Phe Gln Tyr Asn Arg Arg Gly Val Ala Trp Asp Asp Tyr Ile
  115      120      125
Glu Trp Gly His Val Val Ser Gln Asp Leu Val His Trp Arg Pro Leu
  130      135      140
Pro Leu Ala Leu Arg Pro Asp His Trp Tyr Asp Lys Lys Gly Val Leu
  145      150      155      160
Ser Gly Thr Ile Thr Val Leu His Asn Gly Thr Leu Val Leu Leu Tyr
  165      170      175
Thr Gly Val Thr Glu Asp Pro Met Ala Glu Ser Gln Cys Ile Ala Val
  180      185      190
Pro Thr Asp Pro Asn Asp Pro Leu Leu Arg His Trp Thr Lys His Pro
  195      200      205

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Ala Asn Pro Val Leu Ala His Pro Gln Gly Val Gln Gly Met Asp Phe
 210 215 220
 Arg Asp Pro Thr Ser Ala Trp Phe Asp Lys Ser Asp Ala Thr Trp Arg
 225 230 235 240
 Ile Leu Ile Gly Ser Lys Asp Asp Asp Asn Gly Ser His Ala Gly Ile
 245 250 255
 Ala Phe Ile Phe Lys Thr Lys Asp Phe Leu Ser Phe Glu Arg Val Pro
 260 265 270
 Gly Ile Val His Arg Val Glu Gly Thr Gly Met Trp Glu Cys Ile Asp
 275 280 285
 Phe Tyr Pro Val Gly Gly Gly His Asn Ser Ser Ser Glu Glu Leu Tyr
 290 295 300
 Val Ile Lys Ala Ser Met Asp Asp Glu Arg His Asp Tyr Tyr Ser Leu
 305 310 315 320
 Gly Arg Tyr Asp Ala Ala Ala Asn Thr Trp Thr Pro Leu Asp Ala Glu
 325 330 335
 Leu Asp Leu Gly Ile Gly Leu Arg Tyr Asp Trp Gly Lys Leu Tyr Ala
 340 345 350
 Ala Thr Ser Phe Tyr Asp Pro Leu Lys Gln Arg Arg Ile Met Leu Gly
 355 360 365
 Tyr Val Gly Glu Thr Asp Ser Ala Arg Ala Asp Val Ala Lys Gly Trp
 370 375 380
 Ala Ser Leu Gln Ser Ile Pro Arg Thr Val Thr Leu Asp Glu Lys Thr
 385 390 395 400
 Arg Thr Asn Leu Leu Leu Trp Pro Val Glu Glu Val Glu Ala Leu Arg
 405 410 415
 Tyr Asn Ser Thr Asp Leu Ser Gly Ile Thr Val Asp Asn Gly Ser Val
 420 425 430
 Phe His Leu Pro Leu His Gln Ala Thr Gln Leu Asp Ile Glu Ala Ser
 435 440 445
 Phe Arg Leu Asp Ala Ser Asp Val Ala Ala Ile Asn Glu Ala Asp Val
 450 455 460
 Gly Tyr Asn Cys Ser Ser Ser Gly Gly Ala Ala Arg Gly Ala Ile
 465 470 475 480
 Gly Pro Phe Gly Leu Leu Val His Ala Ala Gly Asp Leu Arg Gly Glu
 485 490 495
 Gln Thr Ala Val Tyr Phe Tyr Val Ser Arg Ala Leu Asp Gly Thr Leu
 500 505 510
 Arg Thr Ser Phe Cys Asn Asp Glu Thr Arg Ser Ser Arg Ala Arg Asp
 515 520 525
 Val Thr Lys Arg Val Val Gly Ser Thr Val Pro Val Leu His Gly Glu
 530 535 540
 Ala Leu Ser Met Arg Val Leu Val Asp His Ser Ile Val Gln Ser Phe
 545 550 555 560
 Ala Met Gly Gly Arg Val Thr Ala Thr Ser Arg Val Tyr Pro Thr Glu
 565 570 575
 Ala Ile Tyr Ala Arg Ala Gly Val Tyr Leu Phe Asn Asn Ala Thr Gly
 580 585 590
 Ala Ser Val Thr Ala Glu Arg Leu Ile Val His Glu Met Ala Ser Ala
 595 600 605
 Val Tyr Asp Glu Thr Leu Ile Met Val Glu Asp Ser
 610 615 620

<210> 165

<211> 623

<212> PRT

<213> Festuca arundinacea

<400> 165

Met Glu Ser Arg Ala Phe Pro Ser Ala Ala Tyr Ala Pro Leu Leu Pro
 1 5 10 15
 Ser Ala Ala Asp Asp Val Ala Leu Ala Lys Gln Asp Arg Pro Gly Val
 20 25 30
 Gly Trp Arg Gly Phe Leu Thr Val Leu Ala Ala Cys Gly Val Val Val
 35 40 45

Leu Leu Val Gly Ala Thr Leu Leu Ala Gly Ser Arg Met Gly Gln Ala
 50 55 60
 Gly Asp Gly Glu Gly Asn Thr Asp Glu Asp Gly Ala Gly Gly Phe Pro
 65 70 75 80
 Trp Ser Asn Glu Met Leu Gln Trp Gln Arg Ala Gly Phe His Tyr Gln
 85 90 95
 Pro Glu Gly His Phe Met Ser Asp Pro Asn Gly Pro Val Tyr Tyr Arg
 100 105 110
 Gly Tyr Tyr His Leu Phe Phe Gln Tyr Asn Arg Arg Gly Val Ala Trp
 115 120 125
 Asp Asp Tyr Ile Glu Trp Gly His Val Val Ser Gln Asp Leu Val His
 130 135 140
 Trp Arg Pro Leu Pro Leu Ala Met Arg Pro Asp His Trp Tyr Asp Lys
 145 150 155 160
 Lys Gly Val Leu Ser Gly Thr Ile Thr Val Leu His Asn Gly Thr Leu
 165 170 175
 Val Leu Leu Tyr Thr Gly Val Thr Glu Asp Pro Met Ala Glu Ser Gln
 180 185 190
 Cys Ile Ala Val Pro Thr Asp Pro Asn Asp Pro Leu Leu Arg His Trp
 195 200 205
 Thr Lys His Pro Ala Asn Pro Val Leu Ala His Pro Gln Gly Val Gln
 210 215 220
 Gly Met Asp Phe Arg Asp Pro Thr Ser Ala Trp Trp Asp Lys Ser Asp
 225 230 235 240
 Ala Thr Trp Arg Ile Leu Ile Gly Ser Lys Asp Asp Asp Asn Gly Ser
 245 250 255
 His Ala Gly Ile Ala Phe Ile Phe Lys Thr Lys Asp Phe Leu Ser Phe
 260 265 270
 Glu Arg Val Pro Gly Ile Val His Arg Val Glu Gly Thr Gly Met Trp
 275 280 285
 Glu Cys Ile Asp Phe Tyr Pro Val Gly Gly Gly His Asn Ser Ser Ser
 290 295 300
 Glu Glu Leu Tyr Val Ile Lys Ala Ser Met Asp Asp Glu Arg His Asp
 305 310 315 320
 Tyr Tyr Ser Leu Gly Arg Tyr Asp Ala Ala Ala Asn Thr Trp Thr Pro
 325 330 335
 Leu Asp Ala Glu Leu Asp Leu Gly Ile Gly Leu Arg Tyr Asp Trp Gly
 340 345 350
 Lys Leu Tyr Ala Ser Thr Ser Phe Tyr Asp Pro Val Lys Gln Arg Arg
 355 360 365
 Ile Met Leu Gly Tyr Val Gly Glu Val Asp Ser Ala Arg Ala Asp Val
 370 375 380
 Ala Lys Gly Trp Ala Ser Leu Gln Ser Ile Pro Arg Thr Val Ala Leu
 385 390 395 400
 Asp Glu Lys Thr Arg Thr Asn Leu Leu Leu Trp Pro Val Glu Glu Val
 405 410 415
 Glu Ala Leu Arg Tyr Asn Ser Thr Asp Leu Ser Gly Ile Thr Ile Asp
 420 425 430
 Asn Gly Ser Val Phe His Leu Pro Leu His Gln Thr Thr Gln Leu Asp
 435 440 445
 Ile Glu Ala Ser Phe Arg Leu Asp Ala Ser Asp Val Ala Ala Ile Asn
 450 455 460
 Glu Ala Asp Val Gly Tyr Asn Cys Ser Ser Ser Gly Gly Ala Ala Ala
 465 470 475 480
 Arg Gly Ala Leu Gly Pro Phe Gly Leu Leu Val His Ala Ala Gly Asp
 485 490 495
 Leu Arg Gly Glu Gln Thr Ala Val Tyr Phe Tyr Val Ser Arg Ala Leu
 500 505 510
 Asp Gly Thr Leu Arg Thr Ser Phe Cys Asn Asp Glu Thr Arg Ser Ser
 515 520 525
 Arg Ala Arg Asp Val Thr Lys Arg Val Val Gly Ser Thr Val Pro Val
 530 535 540
 Leu Asp Gly Glu Ala Leu Ser Met Arg Val Leu Val Asp His Ser Ile
 545 550 555 560
 Val Gln Ser Phe Ala Met Gly Gly Arg Thr Thr Ala Thr Ser Arg Val
 565 570 575

Tyr Pro Thr Glu Ala Ile Tyr Ala Arg Ala Gly Val Tyr Leu Phe Asn
 580 585 590
 Asn Ala Thr Gly Ala Gly Val Thr Ala Glu Arg Leu Ile Val His Glu
 595 600 605
 Met Ala Ser Ala Val Tyr Asp Glu Thr Leu Met Val Glu Asp Ser
 610 615 620

<210> 166

<211> 619

<212> PRT

<213> Festuca arundinacea

<400> 166

Met Glu Ser Arg Asp Phe Pro Ser Ala Ala Tyr Ala Pro Leu Leu Pro
 1 5 10 15
 Ser Ala Ala Asp Asp Val Ala Leu Ala Lys Gln Asp Arg Pro Gly Val
 20 25 30
 Gly Trp Arg Gly Phe Leu Thr Val Leu Ala Ala Cys Gly Val Val Val
 35 40 45
 Leu Leu Val Ala Ala Ser Leu Leu Ala Gly Ser Arg Met Gly Gln Ala
 50 55 60
 Gly Asp Thr Asp Glu Asp Gly Ala Gly Gly Phe Pro Trp Ser Asn Glu
 65 70 75 80
 Met Leu Gln Trp Gln Arg Ala Gly Phe His Tyr Gln Pro Glu Gly His
 85 90 95
 Phe Met Ser Asp Pro Asp Gly Pro Val Tyr Tyr Arg Gly Tyr Tyr His
 100 105 110
 Leu Phe Phe Gln Tyr Asn Arg Arg Gly Val Ala Trp Asp Asp Tyr Ile
 115 120 125
 Glu Trp Gly His Val Val Ser Gln Asp Leu Val His Trp Arg Pro Leu
 130 135 140
 Pro Leu Ala Met Arg Pro Asp His Trp Tyr Asp Lys Lys Gly Val Leu
 145 150 155 160
 Ser Gly Thr Ile Thr Val Leu His Asn Gly Thr Leu Val Leu Leu Tyr
 165 170 175
 Thr Gly Val Thr Glu Asp Pro Met Ala Glu Ser Gln Cys Ile Ala Val
 180 185 190
 Pro Thr Asp Pro Asn Asp Pro Leu Leu Arg His Trp Thr Lys His Pro
 195 200 205
 Ala Asn Pro Val Leu Ala His Pro Gln Gly Val Gln Gly Met Asp Phe
 210 215 220
 Arg Asp Pro Thr Ser Ala Trp Trp Asp Lys Ser Asp Ser Thr Trp Arg
 225 230 235 240
 Ile Leu Ile Gly Ser Lys Asp Asp Asp Asn Gly Ser His Ala Gly Ile
 245 250 255
 Ala Phe Ile Phe Lys Thr Lys Asp Phe Leu Ser Phe Glu Arg Val Pro
 260 265 270
 Gly Ile Val His Arg Val Glu Gly Thr Gly Met Trp Glu Cys Ile Asp
 275 280 285
 Phe Tyr Pro Val Gly Gly Gly His Asn Ser Ser Ser Glu Glu Leu Tyr
 290 295 300
 Val Ile Lys Ala Ser Met Asp Asp Glu Arg His Asp Tyr Tyr Ser Leu
 305 310 315 320
 Gly Arg Tyr Asp Ala Ala Ala Asn Thr Trp Thr Pro Leu Asp Ala Glu
 325 330 335
 Leu Asp Leu Gly Ile Gly Leu Arg Tyr Asp Trp Gly Lys Leu Tyr Ala
 340 345 350
 Ser Thr Ser Phe Tyr Asp Pro Leu Lys Gln Arg Arg Ile Met Leu Gly
 355 360 365
 Tyr Val Gly Glu Val Asp Ser Ala Arg Ala Asp Val Ala Lys Gly Trp
 370 375 380
 Ala Ser Leu Gln Ser Ile Pro Arg Thr Val Ala Leu Asp Glu Lys Thr
 385 390 395 400
 Arg Thr Asn Leu Leu Leu Trp Pro Val Glu Glu Val Glu Ala Leu Arg
 405 410 415

Tyr Asn Ser Thr Asp Leu Ser Gly Ile Thr Val Glu Asn Gly Ser Ile
 420 425 430
 Phe His Leu Pro Leu His Gln Ala Thr Gln Leu Asp Ile Glu Ala Ser
 435 440 445
 Phe Arg Leu Asp Ala Ser Asp Val Ala Ala Ile Asn Glu Ala Asp Val
 450 455 460
 Gly Tyr Asn Cys Ser Ser Ser Gly Gly Ala Ala Arg Gly Ala Leu
 465 470 475 480
 Gly Pro Phe Gly Leu Leu Val His Ala Ala Gly Asp Leu Arg Gly Glu
 485 490 495
 Gln Thr Ala Val Tyr Phe Tyr Val Ser Arg Ala Leu Asp Gly Ser Leu
 500 505 510
 Arg Thr Ser Phe Cys Asn Asp Glu Thr Arg Ser Ser Arg Ala Arg Asp
 515 520 525
 Val Thr Lys Arg Val Val Gly Ser Thr Val Pro Val Leu Asp Gly Glu
 530 535 540
 Val Leu Ala Met Arg Val Leu Val Asp His Ser Ile Val Gln Ser Phe
 545 550 555 560
 Ala Met Gly Gly Arg Val Thr Ala Thr Ser Arg Val Tyr Pro Thr Glu
 565 570 575
 Ala Ile Tyr Ala Arg Ala Gly Val Tyr Leu Phe Asn Asn Ala Thr Gly
 580 585 590
 Ala Ser Val Thr Ala Glu Arg Leu Ile Val His Glu Met Ala Ser Ala
 595 600 605
 Val Tyr Asp Glu Thr Val Met Val Lys Asp Ser
 610 615

<210> 167

<211> 1075

<212> PRT

<213> Lolium perenne

<400> 167

Met Ala Gly Asn Asp Trp Ile Asn Ser Tyr Leu Glu Ala Ile Leu Asp
 1 5 10 15
 Ala Gly Gly Thr Ala Gly Asp Ile Ser Ala Ala Ser Val Ala Gly Gly
 20 25 30
 Asp Asp Gly Pro Gly Ala Gly Gly Thr Ala Gly Glu Lys Arg Asp
 35 40 45
 Lys Ser Ser Leu Met Leu Arg Glu Arg Gly Arg Phe Asn Pro Ala Arg
 50 55 60
 Tyr Phe Val Glu Glu Val Ile Ser Gly Phe Asp Glu Thr Asp Leu Tyr
 65 70 75 80
 Lys Thr Trp Val Arg Thr Ser Ala Met Arg Ser Pro Gln Glu Arg Asn
 85 90 95
 Thr Arg Leu Glu Asn Met Ser Trp Arg Ile Trp Asn Leu Ala Arg Lys
 100 105 110
 Lys Lys Gln Ile Glu Gly Glu Glu Ala Ser Arg Leu Ser Lys Lys Arg
 115 120 125
 Leu Glu Arg Glu Lys Ala Arg Arg Asp Ala Ala Ala Asp Leu Ser Glu
 130 135 140
 Asp Leu Ser Glu Gly Glu Lys Gly Glu Asn Ile Asn Gly Ser Ser Val
 145 150 155 160
 His Asp Glu Ser Thr Arg Gly Arg Met Pro Arg Ile Gly Ser Thr Asp
 165 170 175
 Ala Ile Glu Val Trp Ala Asn Gln His Lys Asp Lys Lys Leu Tyr Ile
 180 185 190
 Val Leu Ile Ser Ile His Gly Leu Ile Arg Gly Glu Asn Met Glu Leu
 195 200 205
 Gly Arg Asp Ser Asp Thr Gly Gly Gln Val Lys Tyr Val Val Glu Leu
 210 215 220
 Ala Arg Ala Leu Gly Glu Thr Pro Gly Val Tyr Arg Val Asp Leu Leu
 225 230 235 240
 Thr Arg Gln Ile Ser Ala Pro Asp Val Asp Trp Ser Tyr Gly Glu Pro
 245 250 255

Thr Glu Met Leu Ser Pro Arg Asn Ser Glu Asn Leu Gly Asp Asp Met
 260 265 270
 Gly Glu Ser Ser Gly Ala Tyr Ile Val Arg Ile Pro Phe Gly Pro Arg
 275 280 285
 Glu Lys Tyr Ile Pro Lys Glu Gln Leu Trp Pro His Ile Gln Glu Phe
 290 295 300
 Val Asp Gly Ala Leu Val His Ile Met Gln Met Ser Lys Val Leu Gly
 305 310 315 320
 Glu Gln Val Gly Arg Glu Arg Arg Val Trp Pro Val Val Ile His Gly
 325 330 335
 His Tyr Ala Asp Ala Gly Asp Ser Ala Ala Leu Leu Ser Gly Ala Leu
 340 345 350
 Asn Val Pro Met Val Phe Thr Gly His Ser Leu Gly Arg Asp Lys Leu
 355 360 365
 Glu Gln Leu Leu Lys Gln Gly Arg Gln Thr Arg Asp Glu Val Asn Ala
 370 375 380
 Thr Tyr Lys Ile Met Arg Arg Ile Glu Ala Glu Glu Leu Cys Leu Asp
 385 390 395 400
 Ala Ser Glu Ile Val Ile Thr Ser Thr Arg Gln Glu Ile Glu Lys Gln
 405 410 415
 Trp Gly Leu Tyr Asn Gly Phe Asp Val Thr Met Glu Arg Lys Leu Arg
 420 425 430
 Ala Arg Thr Lys Arg Gly Val Ser Cys Tyr Gly Arg Tyr Met Pro Arg
 435 440 445
 Met Ile Ala Ile Pro Pro Gly Met Glu Phe Ser His Ile Val Pro His
 450 455 460
 Asp Val Asp Leu Asp Gly Asp Glu Ala Asn Glu Val Gly Ser Gly Ser
 465 470 475 480
 Pro Asp Pro Pro Ile Trp Ala Asp Ile Met Arg Phe Phe Ser Asn Pro
 485 490 495
 Arg Lys Pro Met Ile Leu Ala Leu Ala Arg Pro Asp Pro Lys Lys Asn
 500 505 510
 Ile Thr Thr Leu Val Lys Ala Phe Gly Glu His Pro Gly Leu Arg Asn
 515 520 525
 Leu Ala Asn Leu Thr Leu Ile Met Gly Asn Arg Asp Val Ile Asp Glu
 530 535 540
 Met Ser Ser Thr Asn Gly Ala Val Leu Thr Ser Val Leu Lys Leu Ile
 545 550 555 560
 Asp Lys Tyr Asp Leu Tyr Gly Gln Val Ala Tyr Pro Lys His His Lys
 565 570 575
 Gln Ser Glu Val Pro Asp Ile Tyr Arg Leu Ala Ala Arg Thr Lys Gly
 580 585 590
 Val Phe Ile Asn Cys Ala Tyr Ile Glu Pro Phe Gly Leu Thr Leu Ile
 595 600 605
 Glu Ala Ala Ala Tyr Gly Leu Pro Met Val Ala Thr Gln Asn Gly Gly
 610 615 620
 Pro Val Asp Ile His Arg Val Leu Asp Asn Gly Ile Leu Val Asp Pro
 625 630 635 640
 His Asn Gln Asn Asp Ile Ala Glu Ala Leu Tyr Lys Leu Val Ser Asp
 645 650 655
 Lys His Leu Trp Ala Gln Cys Arg Gln Asn Gly Leu Asp Asn Ile His
 660 665 670
 Arg Phe Ser Trp Pro Glu His Cys Lys Asn Tyr Leu Ser Arg Val Gly
 675 680 685
 Thr Val Lys Pro Arg His Pro Arg Trp Gln Arg Ser Asp Asp Ala Thr
 690 695 700
 Glu Val Ser Glu Ser Asp Ser Pro Gly Asp Ser Leu Arg Asp Val His
 705 710 715 720
 Asp Ile Ser Leu Asn Leu Lys Leu Ser Leu Asp Ser Glu Lys Ala Gly
 725 730 735
 Thr Lys Ile Asn Thr Glu Arg Asn Ser Thr Asn Ala Arg Arg Asn Leu
 740 745 750
 Glu Asp Ala Val Leu Lys Phe Ser Asn Ala Val Ser Glu Gly Thr Lys
 755 760 765
 Asp Glu Ser Asp Glu Asn Ala Glu Ala Thr Thr Gly Ser Asn Lys Trp
 770 775 780

Pro Ser Leu Arg Arg Arg Lys His Ile Val Val Ile Ala Val Asp Ser
 785 790 795 800
 Val Gln Asn Ala Asp Leu Val Gln Ile Ile Lys Asn Leu Phe Glu Ala
 805 810 815
 Ser Arg Lys Glu Lys Ser Ser Gly Ala Val Gly Phe Val Leu Ser Thr
 820 825 830
 Ser Arg Ala Ile Ser Glu Thr Leu Thr Phe Leu Thr Ser Gly Gly Ile
 835 840 845
 Gln Thr Thr Glu Phe Asp Ala Phe Ile Cys Ser Ser Gly Ser Asp Leu
 850 855 860
 Cys Tyr Pro Ser Ser Ser Ser Glu Asp Met Leu Ser Pro Thr Glu Leu
 865 870 875 880
 Pro Phe Met Ile Asp Leu Asp Tyr His Ser Gln Ile Glu Tyr Arg Trp
 885 890 895
 Gly Gly Glu Gly Leu Arg Lys Thr Leu Ile Arg Trp Ala Ala Glu Asn
 900 905 910
 Asn Ser Gln Ser Gly Gln Glu Val Thr Glu Asp Glu Glu Cys Ser
 915 920 925
 Ser Thr Tyr Cys Ile Ser Phe Lys Val Lys Asn Thr Glu Ala Val Pro
 930 935 940
 Pro Val Lys Asp Leu Arg Lys Thr Met Arg Ile Gln Ala Leu Arg Cys
 945 950 955 960
 His Val Leu Tyr Ser His Asp Gly Ser Lys Leu Asn Leu Ile Pro Leu
 965 970 975
 Leu Ala Ser Arg Ser Gln Ala Leu Arg Tyr Leu Tyr Ile Arg Trp Gly
 980 985 990
 Val Glu Leu Ala Asn Met Thr Val Val Gly Glu Ser Gly Asp Thr
 995 1000 1005
 Asp Tyr Glu Gly Leu Leu Gly Gly Val His Lys Thr Ile Ile Leu Lys
 1010 1015 1020
 Gly Ser Phe Asn Ala Ala Pro Asn Gln Leu His Ala Ala Arg Ser Tyr
 1025 1030 1035 1040
 Ser Leu Glu Asp Val Ile Ser Phe Asp Lys Pro Gly Ile Ala Ser Val
 1045 1050 1055
 Glu Gly Tyr Leu Pro Asp Ser Leu Lys Ser Ala Leu Gln Gln Phe Gly
 1060 1065 1070
 Val Leu Asn
 1075

<210> 168

<211> 938

<212> PRT

<213> Lolium perenne

<400> 168

Met Ala Ala Gly Asn Glu Trp Ile Asn Gly Tyr Leu Glu Ala Ile Leu
 1 5 10 15
 Asp Ala Gly Ser Lys Leu Arg Pro Gln Gly Val Gln Leu Pro Pro Leu
 20 25 30
 Glu Thr Ala Pro Ala Leu Ala Ala Glu Glu Ser Ser Ala Ala Tyr Asn
 35 40 45
 Pro Thr Arg Tyr Phe Val Glu Glu Val Val Arg Ser Phe Asp Glu Gln
 50 55 60
 Ala Leu His Lys Thr Trp Thr Lys Val Val Ala Met Arg Asn Ser Gln
 65 70 75 80
 Glu Arg Ser Asn Arg Leu Glu Asn Leu Cys Trp Arg Ile Trp Asn Val
 85 90 95
 Ser Arg Gln Lys Lys Gln Val Glu Trp Asp Tyr Thr Lys Glu Val Ala
 100 105 110
 Arg Arg Lys Leu Glu Gln Glu Leu Gly Ser Arg Glu Ala Ala Glu Asp
 115 120 125
 Leu Ser Glu Leu Ser Glu Gly Glu Lys Asp Thr Thr Ala Lys Pro
 130 135 140
 Asp Ala Ala Ala Ala Gln Pro Ser Ala Asp Asp Gly Glu His Gln Gln
 145 150 155 160

Pro Gln Pro Arg Thr Arg Leu Ala Arg Ile Asn Ser Glu Val Arg Leu
 165 170 175
 Val Ser Asp Asp Glu Glu Glu Gln Thr Lys Lys Arg Asn Leu Tyr Ile
 180 185 190
 Val Leu Ile Ser Ile His Gly Leu Val Arg Gly Glu Asn Met Glu Leu
 195 200 205
 Gly Arg Asp Ser Asp Thr Gly Gly Gln Val Lys Tyr Val Val Glu Leu
 210 215 220
 Ala Arg Ala Leu Ala Ala Thr Ala Gly Val His Arg Val Asp Leu Leu
 225 230 235 240
 Thr Arg Gln Ile Ser Cys Pro Asp Val Asp Trp Thr Tyr Gly Glu Pro
 245 250 255
 Val Glu Met Leu Glu Arg Leu Ser Ser Ala Asp Ala Asp Asp Asp
 260 265 270
 Gly Glu Gln Ala Gly Gly Gly Ala Tyr Ile Val Arg Leu Pro Cys Gly
 275 280 285
 Pro Arg Asp Gln Tyr Ile Pro Lys Glu Glu Leu Trp Pro His Ile Pro
 290 295 300
 Glu Phe Val Asp Arg Ala Leu Ser His Val Thr Glu Val Ala Arg Ala
 305 310 315 320
 Leu Gly Glu Gln Leu Gln Pro Pro Pro Ser Pro Ala Asp Gly Ala Val
 325 330 335
 Ala Ala Pro Ile Trp Pro Tyr Val Ile His Gly His Tyr Ala Asp Ala
 340 345 350
 Ala Glu Val Ala Ala Asn Leu Ala Ser Ala Leu Asn Val Pro Met Val
 355 360 365
 Met Thr Gly His Ser Leu Gly Arg Asn Lys Leu Glu Gln Leu Leu Lys
 370 375 380
 Leu Gly Arg Met Pro Gly Pro Glu Ile Gln Gly Thr Tyr Lys Ile Ala
 385 390 395 400
 Arg Arg Ile Glu Ala Glu Glu Thr Gly Leu Asp Thr Ala Glu Met Val
 405 410 415
 Val Thr Ser Thr Lys Gln Glu Ile Glu Glu Gln Trp Gly Leu Tyr Asp
 420 425 430
 Gly Phe Asp Leu Met Val Glu Arg Lys Leu Arg Val Arg Gln Arg Arg
 435 440 445
 Gly Val Ser Ser Leu Gly Arg Tyr Met Pro Arg Met Ala Val Ile Pro
 450 455 460
 Pro Gly Met Asp Phe Ser Phe Val Glu Thr Gln Asp Thr Ala Asp Gly
 465 470 475 480
 Asp Gly Ala Asp Leu Gln Met Leu Ile Ala Pro Asp Lys Ala Lys Lys
 485 490 495
 Ala Leu Pro Pro Ile Trp Ser Asp Val Leu Arg Phe Phe Thr Asn Pro
 500 505 510
 His Lys Pro Met Ile Leu Ala Leu Ser Arg Pro Asp Pro Lys Lys Asn
 515 520 525
 Val Thr Thr Leu Leu Lys Ala Tyr Gly Glu Ser Arg Gln Leu Arg Glu
 530 535 540
 Leu Ala Asn Leu Thr Leu Ile Leu Gly Asn Arg Asp Asp Ile Glu Asp
 545 550 555 560
 Met Ala Gly Gly Gly Gly Ala Val Leu Thr Ala Val Leu Lys Leu Ile
 565 570 575
 Asp Arg Tyr Asp Leu Tyr Gly Gln Val Ala Tyr Pro Lys His His Lys
 580 585 590
 Gln Thr Asp Val Pro His Ile Tyr Arg Leu Ala Ala Lys Thr Lys Gly
 595 600 605
 Val Phe Ile Asn Pro Ala Leu Val Glu Pro Phe Gly Leu Thr Ile Ile
 610 615 620
 Glu Ala Ala Ala Tyr Gly Leu Pro Val Val Ala Thr Lys Asn Gly Gly
 625 630 635 640
 Pro Val Asp Ile Leu Lys Ala Leu His Asn Gly Leu Leu Val Asp Pro
 645 650 655
 His Ser Ala Glu Ala Ile Thr Gly Ala Leu Leu Ser Leu Leu Ala Glu
 660 665 670
 Lys Ser Arg Trp Val Glu Cys Arg Arg Asn Gly Leu Arg Asn Ile His
 675 680 685

```

Arg Phe Ser Trp Pro His His Cys Arg Leu Tyr Leu Ser His Val Ser
690 695 700
Thr Tyr Cys Asp Gln Pro Ser Pro His Gln Pro Leu Arg Val Pro Leu
705 710 715 720
Ala Leu Gly Ser Ser Thr Ser Phe Gly Ala Asp Asp Ser Leu Ser Asp
725 730 735
Ser Leu Arg Gly Leu Ser Leu Gln Ile Ser Val Asp Ala Ser Ser Asp
740 745 750
Leu Asn Ala Ala Asp Ser Ala Ala Ala Ile Met Asp Ala Leu Arg Arg
755 760 765
Arg Pro Ala Ser Glu Lys Pro Ala Ser Ser Gly Ala Arg Ala Leu Gly
770 775 780
Phe Ala Pro Gly Arg Arg Glu Ser Leu Leu Val Val Ala Val Asp Cys
785 790 795 800
Tyr Gly Asp Asp Gly Lys Pro Asp Val Glu Gln Leu Lys Lys Ala Ile
805 810 815
Asp Ala Ala Val Ser Val Gly Glu Cys Ala Gly Ala Lys Gln Gly Tyr
820 825 830
Val Leu Ser Thr Gly Met Thr Ile Pro Glu Ala Ala Glu Ala Ile Lys
835 840 845
Ala Cys Gly Ala Asp Val Ala Ser Phe Asp Ala Leu Ile Cys Ser Ser
850 855 860
Gly Ala Glu Leu Cys Tyr Pro Trp Lys Glu Leu Val Ala Asp Glu Glu
865 870 875 880
Tyr Ser Gly His Val Ala Phe Arg Trp Pro Gly Asp His Val Lys Ser
885 890 895
Ala Val Pro Arg Leu Gly Ser Met Glu Glu Ile Ala Leu Ala Ile Asp
900 905 910
Arg Pro Ala Ser Ser Val His Cys His Ala Tyr Ala Ala Thr Asp Ala
915 920 925
Ser Lys Val Ser Ile Thr Glu His Tyr Leu
930 935

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<210> 169

<211> 808

<212> PRT

<213> Lolium perenne

<400> 169

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Met Ala Ala Lys Leu Thr Arg Leu His Ser Leu Arg Glu Arg Leu Gly
1 5 10 15
Ala Thr Phe Ser Ser His Pro Asn Glu Leu Ile Ala Leu Phe Ser Lys
20 25 30
Tyr Val His Gln Gly Lys Gly Met Leu Gln Arg His Gln Leu Leu Thr
35 40 45
Glu Phe Glu Ala Leu Phe Glu Ala Asp Lys Glu Arg Tyr Ala Pro Phe
50 55 60
Glu Asp Ile Leu Arg Ala Ala Gln Glu Ala Ile Val Leu Pro Pro Trp
65 70 75 80
Val Ala Leu Ala Ile Arg Pro Arg Pro Gly Val Trp Asp Tyr Ile Arg
85 90 95
Val Asn Val Ser Glu Leu Ala Val Glu Glu Leu Thr Val Ser Glu Tyr
100 105 110
Leu Ala Phe Lys Glu Gln Leu Val Asp Glu His Ala Ser Ser Lys Phe
115 120 125
Val Leu Glu Leu Asp Phe Glu Pro Phe Asn Ala Ser Phe Pro Arg Pro
130 135 140
Ser Met Ser Lys Ser Ile Gly Asn Gly Val Gln Phe Leu Asn Arg His
145 150 155 160
Leu Ser Ser Lys Leu Phe Gln Asp Lys Glu Ser Leu Tyr Pro Leu Leu
165 170 175
Asn Phe Leu Lys Ala His Asn His Lys Gly Thr Thr Met Met Leu Asn
180 185 190
Asp Arg Ile Gln Ser Leu Arg Gly Leu Gln Ser Ala Leu Arg Lys Ala
195 200 205

```

Glu	Glu	Tyr	Leu	Thr	Ser	Ile	Pro	Glu	Asp	Thr	Pro	Ser	Ser	Glu	Phe
210						215					220				
Asn	His	Arg	Phe	Gln	Glu	Leu	Gly	Leu	Glu	Lys	Gly	Trp	Gly	Asp	Thr
225					230					235					240
Ala	Lys	Arg	Val	Gln	Asp	Thr	Ile	His	Leu	Leu	Leu	Asp	Leu	Leu	Glu
				245						250					255
Ala	Pro	Asp	Pro	Ala	Ser	Leu	Glu	Lys	Phe	Leu	Gly	Thr	Ile	Pro	Met
			260					265					270		
Met	Phe	Asn	Val	Val	Ile	Leu	Ser	Pro	His	Gly	Tyr	Phe	Ala	Gln	Ser
		275					280					285			
Asn	Val	Leu	Gly	Tyr	Pro	Asp	Thr	Gly	Gly	Gln	Val	Val	Tyr	Ile	Leu
290						295					300				
Asp	Gln	Val	Arg	Ala	Leu	Glu	Asn	Glu	Met	Leu	Leu	Arg	Ile	Lys	Gln
305					310					315					320
Gln	Gly	Leu	Asp	Ile	Thr	Pro	Lys	Ile	Leu	Ile	Val	Thr	Arg	Leu	Leu
				325						330					335
Pro	Asp	Ala	Val	Gly	Thr	Thr	Cys	Gly	Gln	Arg	Leu	Glu	Lys	Val	Ile
			340					345					350		
Gly	Thr	Glu	His	Thr	Asp	Ile	Leu	Arg	Val	Pro	Phe	Arg	Thr	Glu	Lys
		355					360					365			
Gly	Ile	Leu	Arg	Lys	Trp	Ile	Ser	Arg	Phe	Asp	Val	Trp	Pro	Tyr	Leu
370						375					380				
Glu	Thr	Tyr	Thr	Glu	Asp	Val	Ala	Asn	Glu	Leu	Met	Arg	Glu	Met	Gln
385					390					395					400
Thr	Lys	Pro	Asp	Leu	Ile	Ile	Gly	Asn	Tyr	Ser	Asp	Gly	Asn	Leu	Val
				405					410						415
Ala	Thr	Leu	Leu	Ala	His	Lys	Leu	Gly	Val	Thr	Gln	Cys	Thr	Ile	Ala
			420					425					430		
His	Ala	Leu	Glu	Lys	Thr	Lys	Tyr	Pro	Asn	Ser	Asp	Ile	Tyr	Leu	Asp
		435					440					445			
Lys	Phe	Asp	Ser	Gln	Tyr	His	Phe	Ser	Cys	Gln	Phe	Thr	Ala	Asp	Leu
450						455					460				
Ile	Ala	Met	Asn	His	Thr	Asp	Phe	Ile	Ile	Thr	Ser	Thr	Phe	Gln	Glu
465					470					475					480
Ile	Ala	Gly	Ser	Lys	Asp	Ser	Val	Gly	Gln	Tyr	Glu	Ser	His	Ile	Ala
				485					490					495	
Phe	Thr	Leu	Pro	Asp	Leu	Tyr	Arg	Val	Val	His	Gly	Ile	Asp	Val	Phe
			500					505					510		
Asp	Pro	Lys	Phe	Asn	Ile	Val	Ser	Pro	Gly	Ala	Asp	Met	Thr	Val	Tyr
		515					520					525			
Phe	Pro	Tyr	Thr	Glu	Thr	Asp	Lys	Arg	Leu	Thr	Ala	Phe	His	Pro	Glu
		530				535					540				
Ile	Glu	Glu	Leu	Leu	Tyr	Ser	Asp	Val	Glu	Asn	Ser	Glu	His	Lys	Phe
545					550					555					560
Val	Leu	Lys	Asp	Lys	Asn	Lys	Pro	Ile	Ile	Phe	Ser	Met	Ala	Arg	Leu
				565						570					575
Asp	Arg	Val	Lys	Asn	Met	Thr	Gly	Leu	Val	Glu	Met	Phe	Gly	Lys	Asn
			580					585					590		
Ala	His	Leu	Lys	Asp	Leu	Ala	Asn	Leu	Val	Ile	Val	Ala	Gly	Asp	His
			595				600					605			
Gly	Lys	Glu	Ser	Lys	Asp	Arg	Glu	Glu	Gln	Ala	Glu	Phe	Lys	Arg	Met
		610					615					620			
Tyr	Ser	Leu	Ile	Glu	Glu	Tyr	Lys	Leu	Glu	Gly	His	Ile	Arg	Trp	Ile
625					630					635					640
Ser	Ala	Gln	Met	Asn	Arg	Val	Arg	Asn	Ala	Glu	Leu	Tyr	Arg	Tyr	Ile
				645					650					655	
Cys	Asp	Thr	Lys	Gly	Ala	Phe	Val	Gln	Pro	Ala	Phe	Tyr	Glu	Ala	Phe
			660					665					670		
Gly	Leu	Thr	Val	Val	Glu	Ala	Met	Thr	Cys	Gly	Leu	Pro	Thr	Ile	Ala
		675					680					685			
Thr	Cys	His	Gly	Gly	Pro	Ala	Glu	Ile	Ile	Val	Asn	Gly	Val	Ser	Gly
		690				695					700				
Leu	His	Ile	Asp	Pro	Tyr	His	Ser	Asp	Lys	Ala	Ala	Asp	Ile	Leu	Val
705					710					715					720
Asn	Phe	Phe	Glu	Lys	Ser	Thr	Ala	Asp	Pro	Thr	Tyr	Trp	Asp	Lys	Met
				725					730						735

Ser Glu Gly Gly Leu Lys Arg Ile Tyr Glu Lys Tyr Thr Trp Lys Leu
 740 745 750
 Tyr Ser Glu Arg Leu Met Thr Leu Thr Gly Val Tyr Gly Phe Trp Lys
 755 760 765
 Tyr Val Ser Asn Leu Glu Arg Arg Glu Thr Arg Arg Tyr Leu Glu Met
 770 775 780
 Phe Tyr Ala Leu Lys Tyr Arg Ser Leu Ala Ala Val Pro Leu Ala
 785 790 795 800
 Val Asp Gly Glu Asn Thr Asp Asn
 805

<210> 170

<211> 815

<212> PRT

<213> Lolium perenne

<400> 170

Met Gly Glu Ala Ala Gly Asp Arg Val Leu Ser Arg Leu His Ser Val
 1 5 10 15
 Arg Glu Arg Ile Gly Asp Ser Leu Ser Ala His Pro Asn Glu Leu Val
 20 25 30
 Ala Val Phe Thr Arg Leu Val Asn Leu Gly Lys Gly Met Leu Gln Pro
 35 40 45
 His Gln Ile Ile Ala Glu Tyr Asn Thr Ala Ile Pro Glu Ala Glu Arg
 50 55 60
 Glu Lys Leu Lys Asp Gly Ala Phe Glu Asp Val Leu Arg Ala Ala Gln
 65 70 75 80
 Glu Ala Ile Val Ile Ser Pro Trp Val Ala Leu Ala Ile Arg Pro Arg
 85 90 95
 Pro Gly Val Trp Glu Tyr Val Arg Val Asn Val Ser Glu Leu Ala Val
 100 105 110
 Glu Glu Leu Ser Val Pro Glu Tyr Leu Gln Phe Lys Glu Gln Leu Val
 115 120 125
 Glu Gly Ser Asn Lys Asp Phe Val Leu Glu Leu Asp Phe Glu Pro Phe
 130 135 140
 Asn Ala Ser Phe Pro Arg Pro Ser Leu Ser Lys Ser Ile Gly Asn Gly
 145 150 155 160
 Val Gln Phe Leu Asn Arg His Leu Ser Ser Lys Leu Phe His Asp Lys
 165 170 175
 Glu Ser Met Tyr Pro Leu Leu Asn Phe Leu Arg Ala His Asn Tyr Lys
 180 185 190
 Gly Met Pro Met Met Met Asn Asp Arg Val Arg Ser Leu Ser Ala Leu
 195 200 205
 Gln Gly Ala Leu Arg Lys Ala Glu Glu His Leu Ser Gly Leu Pro Ala
 210 215 220
 Asp Thr Pro Tyr Ser Asp Phe His His Arg Phe Gln Glu Leu Gly Leu
 225 230 235 240
 Glu Lys Gly Trp Gly Asp Cys Ala Lys Arg Ala Gln Glu Thr Leu His
 245 250 255
 Leu Leu Leu Asp Leu Leu Glu Ala Pro Asp Pro Ser Thr Leu Glu Lys
 260 265 270
 Phe Leu Gly Thr Ile Pro Met Val Phe Asn Val Val Ile Leu Ser Pro
 275 280 285
 His Gly Tyr Phe Ala Gln Ala Asn Val Leu Gly Tyr Pro Asp Thr Gly
 290 295 300
 Gly Gln Val Val Tyr Ile Leu Asp Gln Val Arg Ala Met Glu Asn Glu
 305 310 315 320
 Met Leu Leu Arg Ile Lys Gln Gln Gly Leu Asp Ile Thr Pro Arg Ile
 325 330 335
 Leu Ile Val Thr Arg Leu Leu Pro Asp Ala Thr Gly Thr Thr Cys Gly
 340 345 350
 Gln Arg Leu Glu Lys Val Leu Gly Thr Glu His Thr His Ile Leu Arg
 355 360 365
 Val Pro Phe Arg Thr Glu Asn Gly Ile Val Arg Lys Trp Ile Ser Arg
 370 375 380
 Phe Glu Val Trp Pro Tyr Leu Glu Thr Phe Thr Asp Asp Val Ala His

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385          390          395          400
Glu Ile Ser Gly Glu Leu Gln Ala Asn Pro Asp Leu Ile Ile Gly Asn
405          410          415
Tyr Ser Asp Gly Asn Leu Val Ala Cys Leu Leu Ala His Lys Met Gly
420          425          430
Val Thr His Cys Thr Ile Ala His Ala Leu Glu Lys Thr Lys Tyr Pro
435          440          445
Asn Ser Asp Leu Tyr Trp Lys Lys Phe Glu Asp His Tyr His Phe Ser
450          455          460
Cys Gln Phe Thr Thr Asp Leu Ile Ala Met Asn His Ala Asp Phe Ile
465          470          475
Ile Thr Ser Thr Phe Gln Glu Ile Ala Gly Asn Lys Asp Thr Val Gly
485          490          495
Gln Tyr Glu Ser His Met Ala Phe Thr Met Pro Gly Met Tyr Arg Val
500          505          510
Val His Gly Ile Asp Val Phe Asp Pro Lys Phe Asn Ile Val Ser Pro
515          520          525
Gly Ala Asp Met Ser Ile Tyr Phe Pro Tyr Ser Glu Ser Gln Arg Arg
530          535          540
Leu Thr Ser Leu His Pro Glu Ile Glu Glu Leu Leu Tyr Ser Asp Val
545          550          555
Asp Asn Asp Glu His Lys Phe Val Leu Lys Asp Arg Asn Lys Pro Ile
565          570          575
Ile Phe Ser Met Ala Arg Leu Asp Arg Val Lys Asn Leu Thr Gly Leu
580          585          590
Val Glu Leu Tyr Gly Arg Asn Pro Arg Leu Gln Glu Leu Val Asn Leu
595          600          605
Val Val Val Cys Gly Asp His Gly Asn Pro Ser Lys Asp Lys Glu Glu
610          615          620
Gln Ala Glu Phe Lys Lys Met Phe Asp Leu Ile Glu Gln Tyr Asn Leu
625          630          635
Asn Gly His Ile Arg Trp Ile Ser Ala Gln Met Asn Arg Val Arg Asn
645          650          655
Ala Glu Leu Tyr Arg Tyr Ile Cys Asp Thr Lys Gly Ala Phe Val Gln
660          665          670
Pro Ala Phe Tyr Glu Ala Phe Gly Leu Thr Val Ile Glu Ala Met Thr
675          680          685
Cys Gly Leu Pro Thr Phe Ala Thr Ala Tyr Gly Gly Pro Ala Glu Ile
690          695          700
Ile Val Asn Gly Val Ser Gly Tyr His Ile Asp Pro Tyr Gln Gly Asp
705          710          715
Lys Ala Ser Ala Leu Leu Val Glu Phe Phe Glu Lys Cys Gln Gly Asp
725          730          735
His Ser His Trp Thr Lys Ile Ser Leu Gly Gly Leu Gln Arg Ile Glu
740          745          750
Glu Lys Tyr Thr Trp Lys Leu Tyr Ser Glu Arg Leu Met Thr Leu Thr
755          760          765
Gly Val Tyr Gly Phe Trp Lys Tyr Val Ser Asn Leu Glu Arg Arg Glu
770          775          780
Thr Arg Arg Tyr Leu Glu Met Leu Tyr Ala Leu Lys Tyr Arg Thr Met
785          790          795
Ala Ser Thr Val Pro Leu Ala Val Glu Gly Glu Pro Ser Ser Lys
805          810          815

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<210> 171

<211> 581

<212> PRT

<213> Festuca arundinacea

<400> 171

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Met Ala Gln Ala Trp Ala Phe Phe Leu Leu Ala Leu Phe Ser Phe Ser
1          5          10          15
Ser Tyr Val Ser Arg Ile Phe Leu Cys Ser Arg Asn Gly Glu Gly Ser
20          25          30
Phe Leu Cys Ala Arg Ala Pro Glu Val Pro Ser Ile Ala Ser Asp Arg
35          40          45

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Tyr Arg Thr Ala Tyr His Phe Gln Pro His Lys Asn Trp Met Asn Asp
50      55      60
Pro Asn Gly Pro Met Tyr Tyr Asn Gly Ile Tyr His Leu Phe Phe Gln
65      70      75      80
His Asn Pro Asn Gly Pro Gln Trp Gly Asp Ile Val Trp Gly His Ser
85      90      95
Val Ser Thr Asp Leu Val Asn Trp Ile Ile Leu Glu Pro Ala Ile Glu
100     105     110
Pro Asp Thr Pro Gly Asp Ile Lys Gly Cys Trp Ser Gly Ser Ala Thr
115     120     125
Val Ile Ser Gly Ser Gln Pro Val Ile Met Tyr Thr Gly Gly Asp Val
130     135     140
Glu Asn His Gln Val Gln Asn Ile Ala Leu Pro Lys Asn Arg Ser Asp
145     150     155     160
Pro Tyr Leu Ile Glu Trp Thr Lys Ala Cys Asn Asn Pro Val Leu Gln
165     170     175
Pro Val Gly Pro Gly Met Asn Pro Gly Glu Phe Arg Asp Pro Thr Thr
180     185     190
Gly Trp Ile Gly Pro Asp Gly Leu Trp Arg Ile Ser Ile Gly Ala Glu
195     200     205
Val Asn Gly Tyr Ser Ala Ala Leu Leu Tyr Lys Ser Glu Asp Phe Leu
210     215     220
Asn Trp Ser Arg Val Asp His Pro Leu Tyr Ser Ser Ser Ala Ser Thr
225     230     235     240
Met Trp Glu Cys Leu Asp Phe Phe Ala Val Leu Pro Gly Ser Asn Gly
245     250     255
Gly Leu Asp Leu Ser Ala Ala Ile Pro Lys Gly Ala Lys His Val Leu
260     265     270
Lys Val Ser Val Asp Gln Cys Asp Lys Tyr Met Ile Gly Val Tyr Asp
275     280     285
Leu Glu His Asp Ala Phe Val Pro Asp Thr Ile Leu Asp Asp Arg Trp
290     295     300
Leu Leu Pro Arg Ile Asp Tyr Gly Asn Tyr Tyr Ala Ser Lys Ser Phe
305     310     315     320
Phe Asp Ser Lys Asn Arg Arg Arg Ile Ile Trp Gly Trp Thr Asn Glu
325     330     335
Ser Asp Ser Ser Ser Asp Asp Val Ala Lys Gly Trp Ala Gly Ile Tyr
340     345     350
Ala Ile Pro Arg Thr Ile Trp Leu Asp Arg Asp Gly Lys Gln Leu Leu
355     360     365
Gln Trp Pro Val Glu Glu Ile Glu Ser Leu Arg Arg Asn Glu Ile Asn
370     375     380
Tyr Gln Gly Leu Asp Leu Glu Lys Gly Asp Leu Tyr Glu Ile Lys Gly
385     390     395     400
Val Asp Thr Leu Gln Ala Asp Val Glu Ile Asp Phe Glu Leu Thr Ser
405     410     415
Ile Asp Asp Ala Asp Ser Phe Asp Pro Ser Trp Leu Leu Asp Pro Glu
420     425     430
Lys His Cys Arg Glu Ala Gly Ala Ser Val His Gly Gly Ile Gly Pro
435     440     445
Phe Gly Leu Val Ile Leu Ala Thr Gly Asp Met Glu Glu His Thr Val
450     455     460
Val His Phe Arg Val Tyr Lys Ser Gln Lys Glu Tyr Met Ile Leu Met
465     470     475     480
Cys Ser Asp Ile Arg Arg Ser Ser Leu Arg Gln Gly Leu Tyr Ala Pro
485     490     495
Ala Tyr Gly Gly Phe Phe Glu Phe Asp Leu Glu Lys Glu Arg Lys Ile
500     505     510
Ser Leu Arg Thr Leu Ile Asp Arg Ser Ala Val Glu Ser Phe Gly Gly
515     520     525
Gly Gly Arg Val Cys Ile Ile Ala Arg Val Tyr Pro Val Ala Ile Val
530     535     540
Asp Asp Gly Ser Ala His Met Tyr Ala Phe Asn Asn Gly Ser Thr Thr
545     550     555     560

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Val Arg Val Pro Gln Ile Arg Ala Trp Ser Met Met Thr Ala Gln Val
 565 570 575
 Asn Leu Lys Lys Gly
 580

<210> 172
 <211> 562
 <212> PRT
 <213> Lolium perenne

<400> 172
 Met Asn Gly Ile Glu His Pro Gly Asn Gly Arg Thr Ala Tyr His Phe
 1 5 10 15
 Gln Pro Ala Lys His Trp Gln Asn Asp Pro Asn Gly Pro Met Tyr His
 20 25 30
 Asn Gly Leu Tyr His Phe Phe Tyr Gln Tyr Asn Pro His Gly Pro Thr
 35 40 45
 Trp Asp Thr Gly Lys Leu Ser Trp Gly His Ser Val Ser Gly Asp Leu
 50 55 60
 Val Asn Trp Ala Ala Leu Asp Asn Ala Leu Asp Pro Thr Ala Pro Phe
 65 70 75 80
 Asp Ala Asn Gly Cys Trp Ser Gly Ser Ala Thr Ile Leu Pro Gly Gly
 85 90 95
 Arg Pro Ala Ile Leu Tyr Thr Gly Ile Asp Ala Asp Lys Val Gln Val
 100 105 110
 Gln Asn Val Ala Phe Ala Lys Asp Pro Ser Asp Pro Leu Leu Arg Glu
 115 120 125
 Trp Glu Lys Pro Ser Cys Asn Pro Val Ile Pro Tyr Pro Ala Asp Val
 130 135 140
 Thr Gly Asn Asn Phe Arg Asp Pro Thr Glu Ala Trp Arg Gly Arg Asp
 145 150 155 160
 Gly Leu Trp Arg Val Gly Ile Val Ala Glu Val Lys Gly Val Gly Ser
 165 170 175
 Leu Leu Val Tyr Arg Ser Ala Asp Phe Leu Arg Trp Gln Arg Asn Ala
 180 185 190
 Ala Pro Leu His Ala Ser Ser Arg Asp Val Pro Val Leu Glu Cys Pro
 195 200 205
 Asp Leu Phe Pro Val Ala Ala Ala Gln Gly Ala Thr Glu Gly Leu
 210 215 220
 Glu Thr Ser Ala Pro Ser Gly Ala Gly Val Arg His Val Leu Lys Leu
 225 230 235 240
 Thr Asp Phe Ala Lys Glu Asp His Tyr Met Val Gly Phe Tyr Asp Asp
 245 250 255
 Val Ala Asp Thr Phe Val Pro Ala Glu Pro Glu Arg Gly Asp Asp Pro
 260 265 270
 Asp Asn Trp Arg Arg Leu Asp His Gly His Leu Tyr Ala Ser Lys Ser
 275 280 285
 Phe Tyr Asp Ala Arg Asn Lys Arg Arg Ile Leu Trp Ala Trp Val Asp
 290 295 300
 Glu Thr Asp Gly Gly Gly Val Ala Arg Gly Trp Ala Gly Ile Gln Ala
 305 310 315 320
 Phe Pro Arg Ala Met Trp Leu Asp Ala Asp Gly Lys Arg Leu Val Gln
 325 330 335
 Trp Pro Val Glu Glu Ile Glu Thr Leu Arg Arg Lys Arg Val Gly Leu
 340 345 350
 Arg Trp Ala Thr Asp Val Glu Ala Gly Gly Arg Lys Glu Ile Ala Gly
 355 360 365
 Ile Val Ser Ser Gln Ala Asp Val Glu Val Val Phe Glu Ile Pro Asn
 370 375 380
 Leu Glu Glu Ala Glu Thr Leu Asp Pro Glu Trp Val Leu Asp Pro Lys
 385 390 395 400
 Gly Leu Cys Ala Ala Lys Gly Ala Ser Val His Gly Gly Val Gly Pro
 405 410 415
 Phe Gly Leu Leu Val Leu Ala Ser Gly Asp Leu Glu Glu His Thr Ala
 420 425 430
 Val Phe Phe Arg Val Phe Lys His Asp Gly Lys Tyr Lys Val Leu Met

```

      435      440      445
Cys Thr Asp Leu Thr Lys Ser Ser Thr Lys Ala Gly Ala His Lys Pro
  450      455      460
Ser Tyr Gly Ala Phe Leu Asp Val Asp Val Glu Lys Asp Lys Phe Ile
  465      470      475      480
Ser Leu Arg Thr Leu Ile Asp His Thr Val Val Glu Ser Phe Gly Asp
      485      490      495
Gly Gly Arg Thr Cys Met Thr Ala Arg Val Tyr Pro Glu His Ala Ala
      500      505      510
Met Gly Ser Thr His Leu Tyr Val Phe Asn Asn Gly Thr Gly Ala Val
      515      520      525
Lys Val Ser Lys Leu Glu Ala Trp Glu Leu Ala Thr Ala Ala Val Asn
      530      535      540
Gly Gly Ser Leu Ala Pro Val Val Val Lys Ala Ser Asp Pro Lys Glu
  545      550      555      560
Ala Leu

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<210> 173

<211> 580

<212> PRT

<213> Festuca arundinacea

<400> 173

```

Met Ala His Ala Trp Ala Phe Phe Leu Leu Ala Leu Phe Ser Phe Ser
  1      5      10      15
Ser Cys Val Ser Lys Leu Phe Ile Tyr Ser Arg Asn Gly Glu Gly Ser
      20      25      30
Phe Leu Cys Thr Arg Ser Pro Glu Val Pro Ser Ile Ala Ser Lys Arg
      35      40      45
Tyr Arg Thr Ala Tyr His Phe Gln Ser Pro Lys Asn Trp Ile Asn Asp
      50      55      60
Pro Cys Gly Pro Met Tyr Tyr Asn Gly Ile Tyr His Glu Phe Tyr Gln
      65      70      75      80
Tyr Asn Pro Gly Gly Thr Ile Ala Ala Asn Ile Val Trp Gly His Ser
      85      90      95
Val Ser Thr Asp Leu Val Asn Trp Ile Gln Leu Glu Pro Ala Ile Val
      100      105      110
Arg Asp Thr Pro Tyr Asp Ile His Gly Cys Trp Thr Gly Ser Ile Thr
      115      120      125
Ile Leu Pro Gly Asp Gln Pro Val Ile Ile Tyr Thr Gly Arg Asp Ser
      130      135      140
Asp Asn His Gln Ser Gln Asn Ile Glu Leu Pro Lys Asn Arg Ser Asp
      145      150      155      160
Pro Tyr Leu Arg Glu Trp Thr Lys Ala Asp Asn Asn Pro Arg Ile Leu
      165      170      175
Pro Val Gly Pro Asp Leu Asn Leu Thr Gln Phe Arg Asp Pro Thr Thr
      180      185      190
Gly Trp Ile Gly Pro Asp Gly Leu Trp Arg Ile Ala Ile Gly Ala Glu
      195      200      205
Leu Asn Gly Tyr Gly Ala Ala Leu Leu Tyr Lys Ser Glu Asp Phe Leu
      210      215      220
Asn Trp Thr Arg Val Asp His Pro Leu Tyr Ser Asp Asn Ala Pro Ser
      225      230      235      240
Met Trp Glu Cys Pro Asp Phe Phe Ala Val Leu Pro Gly Asn Asn Gly
      245      250      255
Gly Leu Asp Leu Ser Ala Ala Ile Pro Lys Gly Ala Lys His Val Leu
      260      265      270
Lys Met Ser Val Asp Tyr Ser Asp Lys Tyr Met Ile Gly Val Tyr Asp
      275      280      285
Leu Lys Arg Asp Ala Phe Val Pro Asp Val Val Leu Asp Asp Arg Arg
      290      295      300
Leu Trp Leu Arg Ile Asp Tyr Gly Thr Phe Tyr Ala Ser Lys Ser Phe
      305      310      315      320
Phe Asp Ser Lys Arg Gly Arg Arg Val Ile Trp Gly Trp Ser Asn Glu
      325      330      335

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<210> 174
<211> 569
<212> PRT
<213> Festuca arundinacea Lolium perenne
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<400>	174															
Met	Ala	Gln	Gly	Trp	Pro	Phe	Phe	Leu	Leu	Val	Leu	Phe	Ser	Ser	Cys	
1				5					10					15		
Val	Ser	Asn	His	Leu	Val	Asn	Gly	Glu	Arg	Val	Phe	Leu	Phe	Pro	Gln	
			20					25					30			
Ser	His	Lys	Val	Ser	Ser	Ile	Val	Ser	Lys	Arg	Tyr	Arg	Thr	Ala	Tyr	
		35					40					45				
His	Phe	Gln	Pro	Pro	Lys	Asn	Trp	Ile	Asn	Gly	Pro	Met	Tyr	Tyr	Asn	
	50					55					60					
Gly	Ile	Tyr	His	Glu	Phe	Tyr	Gln	Tyr	Asn	Pro	Asn	Gly	Ser	Leu	Trp	
65				70						75					80	
Gly	Asn	Ile	Ile	Trp	Gly	His	Ser	Val	Ser	Thr	Asp	Leu	Ile	Asn	Trp	
				85					90					95		
Ile	Pro	Val	Glu	Pro	Ala	Ile	Glu	Arg	Asp	Ile	Pro	Ser	Asp	Ile	Asn	
			100					105					110			
Gly	Cys	Trp	Thr	Gly	Ser	Ala	Thr	Ile	Ile	Ser	Gly	Asp	Gln	Pro	Ile	
		115					120					125				
Ile	Ile	Tyr	Thr	Gly	Ala	Asp	Lys	Glu	Asn	Arg	Gln	Leu	Gln	Asn	Ile	
	130					135					140					
Val	Leu	Pro	Lys	Asn	Lys	Ser	Asp	Pro	Tyr	Leu	Arg	Glu	Trp	Thr	Lys	
145				150						155					160	
Ala	Gly	Asn	Asn	Pro	Val	Ile	Gln	Pro	Val	Gly	Pro	Gly	Leu	Asn	Ala	
				165					170					175		
Ser	Gln	Phe	Arg	Asp	Pro	Thr	Thr	Gly	Trp	Ile	Gly	Pro	Asp	Gly	Leu	
			180					185				190				
Trp	Arg	Ile	Ala	Val	Gly	Ala	Glu	Leu	Asn	Gly	Tyr	Gly	Ala	Ala	Leu	
		195				200						205				
Leu	Tyr	Lys	Ser	Gln	Asp	Phe	Leu	Asn	Trp	Thr	Arg	Val	Asp	His	Pro	

210	215	220
Leu Tyr Ser Ser Asn Ala Ser Ser Met Trp Glu Cys Pro Asp Phe Phe		
225	230	235
Ala Val Leu Pro Gly Asn Ser Gly Gly Leu Asp Leu Ser Ala Glu Ile		
	245	250
Pro Asn Gly Ala Lys His Val Leu Lys Met Ser Leu Asp Ser Cys Asp		
	260	265
Lys Tyr Met Ile Gly Val Tyr Asp Leu Lys Ser Asp Thr Phe Met Pro		
	275	280
Asp Ser Val Leu Asp Asp Arg Arg Leu Trp Ser Arg Ile Asp His Gly		
	290	295
Asn Phe Tyr Ala Ser Lys Ser Phe Phe Asp Ser Lys Lys Gly Arg Arg		
305	310	315
Ile Ile Trp Gly Trp Thr Asn Glu Thr Asp Ser Ser Ser Asp Asp Val		
	325	330
Ala Lys Gly Trp Ala Gly Ile His Ala Ile Pro Arg Thr Ile Trp Leu		
	340	345
Asp Ser Tyr Gly Lys Gln Leu Leu Gln Trp Pro Ile Glu Glu Ile Glu		
	355	360
Ser Leu Arg Arg Asn Glu Ile Ser His Gln Gly Leu Glu Leu Lys Lys		
	370	375
Gly Asp Leu Phe Glu Ile Lys Gly Thr Asp Thr Ser Gln Ala Asp Val		
385	390	395
Glu Val Asp Phe Glu Leu Thr Ser Ile Asp Asn Ala Asp Pro Phe Asp		
	405	410
Pro Ser Trp Leu Leu Asp Val Glu Lys Gln Cys Arg Glu Ala Gly Ala		
	420	425
Ser Val Gln Gly Gly Ile Gly Pro Phe Gly Leu Val Val Leu Ala Ser		
	435	440
Asp Asn Met Glu Glu His Thr Ala Val His Phe Arg Val Tyr Lys Ser		
	450	455
Gln Gln Ser Tyr Met Ile Leu Met Cys Ser Asp Leu Arg Arg Ser Ser		
465	470	475
Leu Arg Ser Gly Met Tyr Thr Pro Ala Tyr Gly Gly Phe Phe Glu Phe		
	485	490
Asp Leu Gln Lys Glu Arg Lys Ile Ser Leu Arg Thr Leu Ile Asp Arg		
	500	505
Ser Ala Val Glu Ser Phe Gly Gly Gly Arg Val Cys Ile Met Ala		
	515	520
Arg Val Tyr Pro Val Val Leu Val Asp Asp Gly Gly Ala His Met Tyr		
	530	535
Ala Phe Asn Asn Gly Ser Thr Thr Val Arg Val Pro Gln Leu Arg Ala		
545	550	555
Trp Ser Met Ser Arg Ala Glu His Lys		
	565	

<210> 175

<211> 588

<212> PRT

<213> Lolium perenne

<400> 175

Met Gly Val Arg Leu Gly Arg Val Ala Trp Ala Cys Pro Ala Val Leu	
1	5
Val Leu Leu Leu Gln Leu Ala Gly Ala Ser His Val Val Tyr Glu Thr	
	20
Ser Leu Leu Glu Thr Glu Ala Ala Ala Thr Val Pro Ala Ser Ile	
	35
Phe Glu Leu Ser Thr Gly Tyr His Phe Arg Pro Gln Lys Asn Trp Ile	
	50
Asn Asp Pro Asn Ala Pro Leu Tyr Tyr Lys Gly Trp Tyr His Leu Phe	
65	70
Phe Gln Tyr Asn Pro Lys Gly Ala Val Trp Gly Asn Ile Val Trp Ala	
	85
His Ser Val Ser Arg Asp Leu Ile Asn Trp Val Ala Leu Glu Thr Ala	
	100
	105
	110

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Leu Ala Pro Ser Ile Asp Ala Asp Lys Tyr Gly Cys Trp Ser Gly Ser
    115      120
Ala Thr Ile Met Pro Asp Gly Thr Pro Val Ile Met Tyr Thr Gly Val
    130      135      140
Ser Arg Pro Asp Val Asn Tyr Glu Val Gln Asn Val Ala Phe Pro Lys
    145      150      155      160
Asn Ser Ser Asp Pro Leu Leu Arg Glu Trp Val Lys Pro Ala His Asn
    165      170      175
Pro Val Ile Val Pro Glu Gly Gly Ile Asn Ala Thr Gln Phe Arg Asp
    180      185      190
Pro Thr Thr Ala Trp Tyr Ala Asp Gly His Trp Arg Ile Leu Val Gly
    195      200      205
Ala Leu Ser Gly Ala Ser Arg Gly Val Ala Tyr Val Tyr Arg Ser Arg
    210      215      220
Asp Phe Arg Arg Trp Thr Arg Val Arg Lys Pro Leu His Ser Ala Pro
    225      230      235      240
Thr Gly Met Trp Glu Cys Pro Asp Phe Tyr Pro Val Thr Val Asp Gly
    245      250      255
Lys Glu Ser Gly Val Asp Thr Ser Val Val Ser Ser Ser Arg Val Lys
    260      265      270
His Val Leu Lys Asn Ser Leu Asp Leu Arg Arg Tyr Asp Tyr Tyr Thr
    275      280      285
Val Gly Thr Tyr Asp Arg Leu Lys Glu Arg Tyr Val Pro Asp Asn Pro
    290      295      300
Ala Gly Asp Lys His His Leu Arg Tyr Asp Tyr Gly Asn Phe Tyr Ala
    305      310      315      320
Ser Lys Thr Phe Tyr Asp Pro Ser Lys Arg Arg Arg Ile Leu Trp Gly
    325      330      335
Trp Ala Asn Glu Ser Asp Thr Ala Val Asp Asp Val Ala Lys Gly Trp
    340      345      350
Ala Gly Ile Gln Ala Ile Pro Arg Lys Val Trp Leu Asp Pro Ser Gly
    355      360      365
Arg Gln Leu Met Gln Trp Pro Val Glu Glu Val Glu Ala Leu Arg Gly
    370      375      380
Lys Lys Pro Val Ser Leu Lys Asp Arg Met Val Lys Arg Gly Glu His
    385      390      395      400
Val Glu Val Thr Gly Leu Gln Thr Ala Gln Ala Asp Val Glu Val Ser
    405      410      415
Phe Glu Val Pro Ser Leu Glu Gly Ala Glu Ala Leu Asp Pro Ala Leu
    420      425      430
Ala Asn Asp Ala Gln Lys Leu Cys Gly Val Lys Gly Ala Asp Val Glu
    435      440      445
Gly Gly Val Gly Pro Phe Gly Leu Trp Val Leu Ala Ser Ser Lys Leu
    450      455      460
Glu Glu Arg Thr Ala Val Phe Phe Arg Val Phe Lys Ala Ala Gly Asn
    465      470      475      480
Val Asn Ser Thr Lys Pro Leu Val Leu Met Cys Ser Asp Pro Thr Lys
    485      490      495
Ser Ser Leu Asn Lys Asn Leu Tyr His Pro Thr Phe Ala Gly Phe Val
    500      505      510
Asp Ile Asp Met Ala Lys Gly Lys Ile Ser Leu Arg Ser Leu Ile Asp
    515      520      525
Gln Ser Val Val Glu Ser Phe Gly Ala Gly Gly Arg Thr Cys Ile Leu
    530      535      540
Ser Arg Val Tyr Pro Ser Leu Ala Ile Gly Arg Asn Ala His Leu His
    545      550      555      560
Val Phe Asn Asn Gly Lys Ala Asp Ile Lys Val Ser Arg Leu Thr Ala
    565      570      575
Trp Glu Met Lys Lys Pro Ala Leu Met Asn Gly Ala
    580      585

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<210> 176

<211> 670

<212> PRT

<213> Lolium perenne

<400> 176

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Met Pro Met Glu Ala Arg Asp Gly Val Ser Met Pro Tyr Ser Tyr Ala
 1          5          10          15
Ala Leu Pro Glu Asp Ala Glu Ala Ala Val Val Gly Arg Gly Arg Arg
      20          25          30
Thr Gly Pro Leu Phe Ala Ala Leu Leu Leu Thr Leu Val Ala Ala Leu
 35          40          45
Leu Ala Val Ala Ala Leu Ala Gly Val Arg Leu Val Gly Glu Leu Pro
 50          55          60
Ala Gly Gly Val Val Met Pro Asn His Pro Met Glu Val Met Asp Val
 65          70          75          80
Ser Gly Ser Arg Gly Pro Glu Ser Gly Val Ser Glu Lys Thr Ser Gly
      85          90          95
Ala Ala Ser Glu Ser Gly Gly Met Leu Gly Ala Asp Ala Gly Ser Asn
      100          105          110
Ala Phe Pro Trp Ser Asn Ala Met Leu Gln Trp Gln Arg Thr Gly Phe
      115          120          125
His Phe Gln Pro Glu Lys Asn Trp Met Asn Asp Pro Asn Gly Pro Val
      130          135          140
Tyr Tyr Lys Gly Trp Tyr His Leu Phe Tyr Gln Tyr Asn Pro Glu Gly
      145          150          155          160
Ala Ile Trp Gly Asn Lys Ile Ala Trp Gly His Ala Val Ser Arg Asp
      165          170          175
Met Leu Arg Trp Arg His Leu Pro Ile Ala Met Phe Pro Asp Gln Trp
      180          185          190
Tyr Asp Ile Asn Gly Ala Trp Ser Gly Ser Ala Thr Val Leu Pro Asp
      195          200          205
Gly Arg Ile Val Met Leu Tyr Thr Gly Ser Thr Asn Ala Ser Val Gln
      210          215          220
Val Gln Cys Leu Ala Phe Pro Ser Asp Pro Ser Asp Pro Leu Leu Thr
      225          230          235          240
Asn Trp Thr Lys Tyr Glu Gly Asn Pro Val Leu Tyr Pro Pro Pro His
      245          250          255
Val Gly Glu Lys Asp Phe Arg Asp Pro Thr Thr Ala Trp Tyr Asp Gly
      260          265          270
Ser Asp Gly Met Trp Arg Ile Val Ile Gly Ser Lys Asp Asn Arg Arg
      275          280          285
Ala Gly Met Ala Leu Thr Tyr Lys Thr Lys Asn Phe His Asp Phe Glu
      290          295          300
Leu Val Pro Gly Val Leu His Arg Val Pro Ala Thr Gly Met Trp Glu
      305          310          315          320
Cys Ile Asp Leu Tyr Pro Val Gly Gly Ala Arg Gly Ile Asp Met Thr
      325          330          335
Glu Ala Val Ala Ala Ala Ser Asn Ser Gly Gly Gly Glu Val Leu His
      340          345          350
Val Met Lys Glu Ser Ser Asp Asp Arg His Asp Tyr Tyr Ala Leu
      355          360          365
Gly Arg Tyr Asp Ala Ala Thr Asn Lys Trp Thr Pro Leu Asp Ala Asp
      370          375          380
Ala Asp Val Gly Ile Gly Leu Arg Tyr Asp Trp Gly Lys Phe Tyr Ala
      385          390          395          400
Ser Lys Thr Phe Tyr Asp Pro Ala Lys Lys Arg Arg Val Leu Trp Gly
      405          410          415
Trp Val Gly Glu Thr Asp Ser Glu Arg Ala Asp Val Ala Lys Gly Trp
      420          425          430
Ala Ser Leu Gln Ser Ile Pro Arg Thr Val Val Leu Asp Thr Lys Thr
      435          440          445
Gly Ser Asn Leu Ile Gln Trp Pro Val Val Glu Val Glu Thr Leu Arg
      450          455          460
Thr Asn Ser Thr Asn Leu Gly Ser Ile Ile Val Glu His Gly Ser Val
      465          470          475          480
Phe Pro Leu Ser Leu His Arg Ala Thr Gln Leu Asp Ile Glu Ala Ser
      485          490          495
Phe Arg Leu Asp Pro Leu Asp Val Ala Ala Ala Lys Glu Ala Asp Val
      500          505          510
Gly Tyr Asn Cys Ser Thr Ser Gly Gly Ala Ala Gly Arg Gly Ala Leu

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<div><400> 177</div>	Met	His	Ala	Asp	Pro	Asn	Gly	Pro	Val	Tyr	Tyr	Arg	Gly	Trp	Tyr	His
1				5						10					15	
Leu	Phe	Tyr	Gln	Tyr	Asn	Pro	Glu	Gly	Ala	Val	Trp	Gly	Asn	Ile	Ala	
			20					25					30			
Trp	Gly	His	Ala	Val	Ser	Arg	Asp	Leu	Val	His	Trp	Arg	His	Leu	Pro	
		35					40					45				
Leu	Ala	Met	Val	Pro	Asp	Gln	Trp	Tyr	Asp	Ile	Asn	Gly	Val	Trp	Thr	
	50					55					60					
Gly	Ser	Ala	Thr	Val	Phe	Pro	Asp	Gly	Thr	Leu	Asn	Met	Leu	Tyr	Thr	
65					70					75					80	
Gly	Ser	Thr	Asn	Ala	Ser	Val	Gln	Ala	Gln	Cys	Leu	Ala	Val	Pro	Glu	
			85						90					95		
Asp	Pro	Asn	Asp	Ser	Leu	Leu	Arg	Asn	Trp	Thr	Lys	His	Glu	Ala	Asn	
			100					105					110			
Pro	Val	Leu	Leu	Pro	Pro	Pro	Gly	Ile	Gly	Asp	Lys	Asp	Phe	Arg	Asp	
		115					120					125				
Pro	Thr	Thr	Ala	Trp	Phe	Asp	Glu	Ser	Asp	Gln	Thr	Trp	Arg	Thr	Val	
		130				135					140					
Ile	Gly	Ser	Lys	Asp	Asn	Asn	Gly	His	Ala	Gly	Ile	Ala	Met	Val	Tyr	
145					150					155					160	
Lys	Thr	Lys	Asp	Phe	Leu	Asn	Tyr	Glu	Leu	Ile	Pro	Gly	Tyr	Leu	His	
				165					170					175		
Arg	Val	Asp	Gly	Thr	Gly	Met	Trp	Glu	Cys	Ile	Asp	Phe	Tyr	Pro	Val	
			180					185					190			
Gly	Gly	Lys	Asn	Gly	Ser	Glu	Glu	Leu	Tyr	Val	Ile	Lys	Glu	Ser	Ser	
		195					200					205				
Asp	Asp	Asp	Arg	His	Asp	Trp	Tyr	Thr	Leu	Gly	Lys	Tyr	Asp	Ala	Ala	
		210				215					220					
Ala	Asn	Thr	Phe	Thr	Ala	Ala	Asp	Pro	Glu	Asn	Asp	Leu	Gly	Ile	Gly	
225					230					235					240	
Leu	Arg	Tyr	Asp	Trp	Gly	Lys	Phe	Tyr	Ala	Ser	Lys	Thr	Phe	Tyr	Asp	
				245					250					255		
Pro	Ala	Lys	Lys	Arg	Arg	Val	Leu	Trp	Gly	Trp	Ile	Gly	Glu	Thr	Asp	
			260					265					270			
Ser	Glu	Arg	Ala	Asp	Val	Ala	Lys	Gly	Trp	Ala	Ser	Leu	Met	Ser	Ile	
		275					280					285				
Pro	Arg	Thr	Val	Glu	Leu	Asp	Glu	Lys	Thr	Trp	Thr	Asn	Leu	Ile	Gln	
		290				295						300				
Trp	Pro	Val	Glu	Glu	Ile	Glu	Thr	Leu	Arg	Ile	Lys	Ser	Thr	Asp	Leu	
305					310					315					320	

Gly Gly Ile Thr Ile Asp His Gly Ser Val Tyr Pro Leu Pro Leu His
 325 330 335
 Arg Ala Thr Gln Leu Asp Ile Glu Ala Ser Phe Arg Leu Asp Ala Ala
 340 345 350
 Thr Val Ala Ala Leu Asn Glu Ala Asp Val Gly Tyr Asn Cys Ser Thr
 355 360 365
 Ser Gly Gly Ser Thr His Arg Gly Ala Leu Gly Pro Phe Gly Ile Leu
 370 375 380
 Val Leu Ala Asp Gly Lys Ala Glu Gln Thr Ala Val Tyr Phe Tyr Val
 385 390 395 400
 Ser Lys Gly Leu Asp Gly Ala Leu Glu Thr His Phe Cys His Asp Glu
 405 410 415
 Ser Arg Ser Thr Leu Ala Lys Asp Val Val Lys Arg Val Val Gly Tyr
 420 425 430
 Thr Val Pro Val Leu Asp Gly Glu Ala Phe Ser Val Arg Val Leu Val
 435 440 445
 Asp His Ser Ile Val Glu Ser Phe Ala Met Gly Gly Arg Ser Thr Ala
 450 455 460
 Thr Ser Arg Val Tyr Pro Thr Glu Ser Ile Tyr Gly Ala Ala Gly Ala
 465 470 475 480
 Tyr Leu Phe Asn Asn Ala Thr Gly Gly Ser Val Thr Val Glu Lys Leu
 485 490 495
 Val Val His Glu Met Asp Ser Ser Tyr Asn Gln Ile Phe Met Ala Asp
 500 505 510
 Asp Leu

<210> 178

<211> 557

<212> PRT

<213> Lolium perenne

<400> 178

Met Gly Ser Val Pro Glu Glu Ser Val Val Ser Val Ala Ala Ala Glu
 1 5 10 15
 Thr Val Phe Arg Ser Lys Leu Pro Asp Ile Glu Ile Asn Asn Glu Gln
 20 25 30
 Thr Leu Gln Ser Tyr Cys Phe Glu Lys Met Ala Glu Val Ala Ser Arg
 35 40 45
 Pro Cys Ile Ile Asp Gly Gln Thr Gly Ala Ser Tyr Thr Tyr Thr Glu
 50 55 60
 Val Asp Ser Leu Thr Arg Arg Ala Ala Ala Gly Leu Arg Arg Met Gly
 65 70 75 80
 Val Gly Lys Gly Asp Val Val Met Asn Leu Leu Arg Asn Cys Pro Glu
 85 90 95
 Phe Ala Phe Ser Phe Leu Gly Ala Ala Arg Leu Gly Ala Ala Thr Thr
 100 105 110
 Thr Ala Asn Pro Phe Tyr Thr Pro His Glu Ile His Arg Gln Ala Glu
 115 120 125
 Ala Ala Gly Ala Lys Leu Ile Val Thr Glu Ala Cys Ala Val Glu Lys
 130 135 140
 Val Leu Glu Phe Ala Ala Gly Arg Gly Leu Pro Val Val Thr Val Asp
 145 150 155 160
 Gly Arg Arg Asp Gly Cys Val Asp Phe Ala Glu Leu Ile Ala Gly Glu
 165 170 175
 Glu Leu Pro Glu Ala Asp Glu Ala Gly Ile Leu Pro Asp Asp Val Val
 180 185 190
 Ala Leu Pro Tyr Ser Ser Gly Thr Thr Gly Leu Pro Lys Gly Val Met
 195 200 205
 Leu Thr His Arg Ser Leu Val Thr Ser Val Ala Gln Leu Val Asp Gly
 210 215 220
 Ser Asn Pro Asn Val Cys Phe Asn Lys Asp Asp Ala Leu Leu Cys Leu
 225 230 235 240
 Leu Pro Leu Phe His Ile Tyr Ser Leu His Thr Val Leu Leu Ala Gly
 245 250 255
 Leu Arg Val Gly Ala Ala Ile Val Ile Met Arg Lys Phe Asp Val Gly

			260					265					270		
Ala	Leu	Val	Asp	Leu	Val	Arg	Ala	His	Arg	Ile	Thr	Ile	Ala	Pro	Phe
		275					280					285			
Val	Pro	Pro	Ile	Val	Val	Glu	Ile	Ala	Lys	Ser	Asp	Arg	Val	Gly	Ala
		290				295					300				
Asp	Asp	Leu	Ala	Ser	Ile	Arg	Met	Val	Leu	Ser	Gly	Ala	Ala	Pro	Met
305					310					315					320
Gly	Lys	Asp	Leu	Gln	Asp	Ala	Phe	Met	Ala	Lys	Ile	Pro	Asn	Ala	Val
				325					330					335	
Leu	Gly	Gln	Gly	Tyr	Gly	Met	Thr	Glu	Ala	Gly	Pro	Val	Leu	Ala	Met
			340					345					350		
Cys	Leu	Ala	Phe	Ala	Lys	Glu	Pro	Phe	Lys	Val	Lys	Ser	Gly	Ser	Cys
		355				360					365				
Gly	Thr	Val	Val	Arg	Asn	Ala	Glu	Leu	Lys	Val	Val	Asp	Pro	Asp	Thr
		370			375						380				
Gly	Ala	Ser	Leu	Gly	Arg	Asn	Gln	Pro	Gly	Glu	Ile	Cys	Val	Arg	Gly
385					390					395					400
Lys	Gln	Ile	Met	Ile	Gly	Tyr	Leu	Asn	Asp	Pro	Glu	Ser	Thr	Lys	Asn
			405						410					415	
Thr	Ile	Asp	Lys	Asp	Gly	Trp	Leu	His	Thr	Gly	Asp	Ile	Gly	Leu	Val
			420					425					430		
Asp	Asp	Asp	Asp	Glu	Ile	Phe	Ile	Val	Asp	Arg	Leu	Lys	Glu	Ile	Ile
		435				440					445				
Lys	Tyr	Lys	Gly	Phe	Gln	Val	Ala	Pro	Ala	Glu	Leu	Glu	Ala	Leu	Leu
		450			455					460					
Leu	Thr	Asn	Pro	Glu	Val	Lys	Asp	Ala	Ala	Val	Val	Gly	Val	Lys	Asp
465				470						475					480
Asp	Leu	Cys	Gly	Glu	Val	Pro	Val	Ala	Phe	Ile	Lys	Arg	Ile	Glu	Gly
			485						490					495	
Ser	Glu	Ile	Thr	Glu	Asn	Glu	Ile	Lys	Gln	Phe	Val	Ser	Lys	Glu	Val
			500					505					510		
Val	Phe	Tyr	Lys	Arg	Ile	Asn	Lys	Val	Tyr	Phe	Thr	Asp	Ser	Ile	Pro
		515				520					525				
Lys	Asn	Pro	Ser	Gly	Lys	Ile	Leu	Arg	Lys	Asp	Leu	Arg	Ala	Arg	Leu
		530			535					540					
Ala	Ala	Gly	Ile	Pro	Thr	Glu	Val	Ala	Ala	Pro	Arg	Ser			
545					550					555					

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<210> 179
<211> 501
<212> PRT
<213> Lolium perenne
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<400>	179															
Met	Glu	Val	Leu	Leu	Leu	Glu	Lys	Ala	Leu	Leu	Gly	Leu	Phe	Ala	Ala	
1				5					10					15		
Ala	Val	Leu	Ala	Ile	Ala	Val	Ala	Lys	Leu	Ala	Gly	Lys	Arg	Phe	Arg	
			20					25					30			
Leu	Pro	Pro	Gly	Pro	Ser	Gly	Ala	Pro	Ile	Val	Gly	Asn	Trp	Leu	Gln	
		35					40					45				
Val	Gly	Asp	Asp	Leu	Asn	His	Arg	Asn	Leu	Met	Gly	Ile	Ala	Lys	Arg	
	50					55					60					
Phe	Gly	Glu	Val	Phe	Leu	Leu	Arg	Met	Gly	Ile	Arg	Asn	Leu	Val	Val	
65					70					75					80	
Val	Ser	Ser	Pro	Glu	Leu	Ala	Lys	Glu	Val	Leu	His	Thr	Gln	Gly	Val	
				85					90					95		
Glu	Phe	Gly	Ser	Arg	Thr	Arg	Asn	Val	Val	Phe	Asp	Ile	Phe	Thr	Gly	
			100					105					110			
Asn	Gly	Gln	Asp	Met	Val	Phe	Thr	Val	Tyr	Gly	Asp	His	Trp	Arg	Lys	
		115					120					125				
Met	Arg	Arg	Ile	Met	Thr	Val	Pro	Phe	Phe	Thr	Asn	Lys	Val	Val	Ala	
	130					135					140					
Gln	Asn	Arg	Val	Gly	Trp	Glu	Glu	Glu	Ala	Arg	Leu	Val	Val	Glu	Asp	
145					150					155					160	
Val	Lys	Ala	Asp	Pro	Ala	Ser	Ala	Thr	Ala	Gly	Thr	Val	Ile	Arg	Arg	
				165					170					175		

Arg Leu Gln Leu Met Met Tyr Asn Asp Met Phe Arg Ile Met Phe Asp
 180 185 190
 Arg Arg Phe Glu Ser Val Asp Asp Pro Leu Phe Asn Lys Leu Lys Ala
 195 200 205
 Met Asn Ala Glu Arg Ser Ile Leu Ser Gln Ser Phe Asp Tyr Asn Tyr
 210 215 220
 Gly Asp Phe Ile Pro Ile Leu Arg Pro Phe Leu Arg Lys Tyr Leu Asn
 225 230 235 240
 Arg Cys Thr Asn Leu Lys Thr Lys Arg Met Lys Leu Phe Glu Asp His
 245 250 255
 Phe Val Ala Asp Arg Lys Lys Ala Leu Glu Gln Asn Gly Glu Ile Arg
 260 265 270
 Cys Ala Met Asp His Ile Leu Glu Ala Glu Arg Lys Gly Glu Ile Asn
 275 280 285
 His Asp Asn Val Leu Tyr Ile Val Glu Asn Ile Asn Val Ala Ala Ile
 290 295 300
 Glu Thr Thr Leu Trp Ser Ile Glu Trp Gly Ile Ala Glu Leu Val Asn
 305 310 315 320
 His Pro Asp Val Gln Ser Lys Leu Arg Asp Glu Met Thr Ala Val Leu
 325 330 335
 Gly Ala Asp Val Ala Val Thr Glu Pro Asp Leu Glu Arg Leu Pro Tyr
 340 345 350
 Leu Gln Ser Val Val Lys Glu Thr Leu Arg Leu Arg Met Ala Ile Pro
 355 360 365
 Leu Leu Val Pro His Met Asn Leu Ser Asp Ala Lys Leu Ala Gly Tyr
 370 375 380
 Asp Ile Pro Ala Glu Ser Lys Ile Leu Val Asn Ala Trp Phe Leu Ala
 385 390 395 400
 Asn Asp Pro Lys Arg Trp Val Arg Ala Asp Glu Phe Arg Pro Glu Arg
 405 410 415
 Phe Leu Glu Glu Glu Lys Ala Val Glu Ala His Gly Asn Asp Phe Arg
 420 425 430
 Phe Val Pro Phe Gly Val Gly Arg Ser Cys Pro Gly Ile Val Leu
 435 440 445
 Ala Leu Pro Ile Ile Gly Ile Thr Leu Gly Arg Leu Val Gln Asn Phe
 450 455 460
 Gln Leu Leu Pro Pro Pro Gly Gln Asp Lys Ile Asp Thr Thr Glu Lys
 465 470 475 480
 Pro Gly Gln Phe Ser Asn Gln Ile Leu Lys His Ala Thr Val Val Cys
 485 490 495
 Lys Pro Leu Glu Ala
 500

<210> 180

<211> 361

<212> PRT

<213> Lolium perenne

<400> 180

Met Gly Ser Val Asp Ala Ser Glu Lys Thr Ile Thr Gly Trp Ala Ala
 1 5 10 15
 Arg Asp Ala Thr Gly His Leu Ser Pro Tyr Thr Tyr Asn Leu Arg Arg
 20 25 30
 Thr Gly Ala Glu Asp Val Val Leu Lys Val Leu Tyr Cys Gly Ile Cys
 35 40 45
 His Thr Asp Leu His Gln Thr Lys Asn His Leu Gly Ala Ser Lys Tyr
 50 55 60
 Pro Met Val Pro Gly His Glu Val Val Gly Glu Val Val Glu Val Gly
 65 70 75 80
 Pro Glu Val Ser Lys Tyr Ser Val Gly Asp Val Val Gly Val Gly Val
 85 90 95
 Ile Val Gly Cys Arg Asp Cys Arg Pro Cys Lys Ala Asn Val Glu
 100 105 110
 Gln Tyr Cys Asn Lys Lys Ile Trp Ser Tyr Asn Asp Val Tyr Thr Asp
 115 120 125
 Gly Lys Pro Thr Gln Gly Gly Phe Ala Ser Ser Met Val Val Asp Gln

130	135	140
Lys Phe Val Val Lys Ile Pro Ala Gly Leu Ala Pro Glu Gln Ala Ala		
145	150	155
Pro Leu Leu Cys Ala Gly Val Thr Val Tyr Ser Pro Leu Lys His Phe		160
	165	170
Gly Leu Met Thr Pro Gly Leu Arg Gly Gly Ile Leu Gly Leu Gly Gly		175
	180	185
Val Gly His Met Gly Val Lys Val Ala Lys Ser Met Gly His His Val		190
	195	200
Thr Val Ile Ser Ser Ser Asp Lys Lys Arg Ala Glu Ala Met Asp Asp		205
	210	215
Leu Gly Ala Asp Ala Tyr Leu Val Ser Ser Asp Glu Ala Gln Met Ala		220
225	230	235
Ala Ala Met Asp Ser Leu Asp Tyr Ile Ile Asp Thr Val Pro Val Lys		240
	245	250
His Pro Leu Glu Pro Tyr Leu Ala Leu Leu Lys Met Asp Gly Lys Leu		255
	260	265
Val Leu Met Gly Val Ile Gly Glu Pro Leu Ser Phe Val Ser Pro Met		270
	275	280
Val Met Leu Gly Arg Lys Thr Ile Thr Gly Ser Phe Ile Gly Ser Ile		285
	290	295
Glu Glu Thr Glu Glu Val Leu Arg Phe Cys Val Asp Lys Gly Leu Thr		300
305	310	315
Ser Gln Ile Glu Val Val Lys Met Asp Tyr Leu Asn Gln Ala Leu Glu		320
	325	330
Arg Leu Glu Arg Asn Asp Val Arg Tyr Arg Phe Val Val Asp Val Ala		335
	340	345
Gly Ser Asn Ile Asp Asp Thr Ala Ala		350
	355	360

<210> 181

<211> 363

<212> PRT

<213> Lolium perenne

<400> 181

Met Thr Val Val Glu Val Leu Ala Ala Gly Asp Ala Ala Ala Ala Ala	
1	5
Val Ala Arg Pro Ala Gly Asn Gly Gln Thr Val Cys Val Thr Gly Ala	10
	20
Ala Gly Tyr Ile Ala Ser Trp Leu Val Lys Leu Leu Leu Glu Lys Gly	25
	30
Tyr Thr Val Lys Gly Thr Val Arg Asn Pro Asp Asp Pro Lys Asn Ala	35
	40
His Leu Arg Ala Leu Asp Gly Ala Ala Asp Arg Leu Val Leu Cys Lys	45
65	55
Ala Asp Leu Leu Asp Tyr Asp Ala Ile Arg Arg Ala Ile Asp Gly Cys	60
	70
His Gly Val Phe His Thr Ala Ser Pro Val Thr Asp Asp Pro Glu Gln	75
	85
Met Val Glu Pro Ala Val Arg Gly Thr Gln Tyr Val Ile Asp Ala Ala	90
	100
Ala Glu Ala Gly Thr Val Arg Arg Met Val Leu Thr Ser Ser Ile Gly	105
	110
Ala Val Thr Met Asp Pro Asn Arg Gly Pro Asp Val Val Val Asp Glu	115
145	120
Ser Cys Trp Ser Asp Leu Asp Phe Cys Lys Lys Thr Arg Asn Trp Tyr	125
	135
Cys Tyr Gly Lys Ala Val Ala Glu Gln Ala Ala Ser Glu Leu Ala Arg	140
	150
Gln Arg Gly Val Asp Leu Val Val Asn Pro Val Leu Val Ile Gly	155
	165
Pro Leu Leu Gln Pro Thr Val Asn Ala Ser Ile Gly His Ile Leu Lys	170
	180
Tyr Leu Asp Gly Ser Ala Ser Lys Phe Ala Asn Ala Val Gln Ala Tyr	185
225	195
	200
	210
	215
	220
	230
	235
	240

Val Asp Val Arg Asp Val Ala Asp Ala His Leu Arg Val Phe Glu Cys
 245 250 255
 Ala Ala Ala Ser Gly Arg His Leu Cys Ala Glu Arg Val Leu His Arg
 260 265 270
 Glu Asp Val Val Arg Ile Leu Ala Lys Leu Phe Pro Glu Tyr Pro Val
 275 280 285
 Pro Thr Arg Cys Ser Asp Glu Ala Asn Pro Arg Lys Gln Pro Tyr Lys
 290 295 300
 Met Ser Asn Gln Lys Leu Gln Asp Leu Gly Leu Glu Phe Arg Pro Val
 305 310 315 320
 Ser Gln Ser Leu Tyr Glu Thr Val Lys Ser Leu Gln Glu Lys Gly His
 325 330 335
 Leu Pro Val Leu Ser Glu Gln Ala Glu Ala Asp Lys Glu Thr Leu Ala
 340 345 350
 Ala Glu Leu Gln Ala Gly Val Thr Ile Arg Ala
 355 360

<210> 182

<211> 360

<212> PRT

<213> Festuca arundinacea

<400> 182

Met Gly Ser Thr Ala Ala Asp Met Ala Ala Ser Ala Asp Glu Glu Ala
 1 5 10 15
 Cys Met Phe Ala Leu Gln Leu Ala Ser Ser Ser Ile Leu Pro Met Thr
 20 25 30
 Leu Lys Asn Ala Ile Glu Leu Gly Leu Leu Glu Ile Leu Val Ala Ala
 35 40 45
 Gly Gly Lys Ser Leu Thr Pro Thr Glu Val Ala Ala Lys Leu Pro Ser
 50 55 60
 Ala Ala Asn Pro Glu Ala Pro Asp Met Val Asp Arg Met Leu Arg Leu
 65 70 75 80
 Leu Ala Ser Tyr Asn Val Val Thr Cys Leu Val Glu Glu Gly Lys Asp
 85 90 95
 Gly Arg Leu Ser Arg Ser Tyr Gly Ala Ala Pro Val Cys Lys Phe Leu
 100 105 110
 Thr Pro Asn Glu Asp Gly Val Ser Met Ala Ala Leu Ala Leu Met Asn
 115 120 125
 Gln Asp Lys Val Leu Met Glu Ser Trp Tyr Tyr Leu Lys Asp Ala Val
 130 135 140
 Leu Asp Gly Gly Ile Pro Phe Asn Lys Ala Tyr Gly Met Ser Ala Phe
 145 150 155 160
 Glu Tyr His Gly Thr Asp Pro Arg Phe Asn Arg Val Phe Asn Glu Gly
 165 170 175
 Met Lys Asn His Ser Ile Ile Ile Thr Lys Lys Leu Leu Glu Leu Tyr
 180 185 190
 His Gly Phe Gln Gly Leu Gly Thr Leu Val Asp Val Gly Gly Gly Val
 195 200 205
 Gly Ala Thr Val Ala Ala Ile Ala Ala His Tyr Pro Ala Ile Lys Gly
 210 215 220
 Val Asn Phe Asp Leu Pro His Val Ile Ser Glu Ala Pro Gln Phe Pro
 225 230 235 240
 Gly Val Thr His Val Gly Gly Asp Met Phe Lys Glu Val Pro Ser Gly
 245 250 255
 Asp Ala Ile Leu Met Lys Trp Ile Leu His Asp Trp Ser Asp Gln His
 260 265 270
 Cys Ala Thr Leu Leu Lys Asn Cys Tyr Asp Ala Leu Pro Ala His Gly
 275 280 285
 Lys Val Val Leu Val Glu Cys Ile Leu Pro Val Asn Pro Glu Ala Lys
 290 295 300
 Pro Ser Ser Gln Gly Val Phe His Val Asp Met Ile Met Leu Ala His
 305 310 315 320
 Asn Pro Gly Gly Arg Glu Arg Tyr Glu Arg Glu Phe Glu Ala Leu Ala
 325 330 335

Arg Gly Ala Gly Phe Thr Gly Val Lys Ser Thr Tyr Ile Tyr Ala Asn
340 345 350
Ala Trp Ala Ile Glu Phe Thr Lys
355 360

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<210> 183
<211> 543
<212> PRT
<213> Lolium perenne
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Met	Val	Gly	Phe	Ala	Lys	Ile	Ala	Met	Glu	Trp	Ile	Gln	Asp	Pro	Leu
1			5						10					15	
Ser	Trp	Leu	Phe	Ile	Ala	Ser	Val	Val	Phe	Val	Val	Leu	Gln	Arg	Arg
			20					25					30		
Arg	Arg	Gly	Asn	Val	Ala	Pro	Phe	Pro	Pro	Gly	Pro	Lys	Pro	Leu	Pro
		35					40					45			
Ile	Val	Gly	Asn	Met	Ser	Met	Met	Asp	Gln	Leu	Thr	His	Arg	Gly	Leu
	50					55					60				
Ala	Ala	Leu	Ala	Lys	Glu	Tyr	Gly	Gly	Leu	Leu	His	Ile	Arg	Leu	Gly
65					70					75					80
Lys	Leu	His	Thr	Phe	Ala	Val	Ser	Thr	Pro	Glu	Tyr	Ala	Arg	Glu	Val
				85					90					95	
Leu	Gln	Val	Gln	Asp	Gly	Ala	Phe	Ser	Asn	Arg	Pro	Ala	Thr	Ile	Ala
			100					105					110		
Ile	Ala	Tyr	Leu	Thr	Tyr	Asp	Arg	Ala	Asp	Met	Ala	Phe	Ala	His	Tyr
		115					120					125			
Gly	Pro	Phe	Trp	Arg	Gln	Met	Arg	Lys	Leu	Cys	Val	Met	Lys	Leu	Phe
	130					135					140				
Ser	Arg	Arg	Arg	Pro	Glu	Thr	Trp	Leu	Ala	Val	Arg	Asp	Glu	Ser	Ala
145					150					155					160
Ala	Leu	Val	Arg	Ala	Val	Ala	Arg	Arg	Thr	Gly	Glu	Ser	Val	Asp	Leu
				165					170					175	
Gly	Glu	Leu	Ile	Phe	Lys	Leu	Thr	Lys	Asn	Val	Ile	Phe	Arg	Ala	Ala
			180					185					190		
Phe	Gly	Ala	Gly	Ala	Val	Ala	Ala	Asp	Ala	Glu	Glu	Gly	Asp	Gly	Ala
		195					200					205			
Gly	Lys	Gln	Asp	Glu	Phe	Ile	Ala	Ile	Leu	Gln	Glu	Phe	Ser	Lys	Leu
	210					215					220				
Phe	Gly	Ala	Phe	Asn	Ile	Gly	Asp	Phe	Ile	Pro	Trp	Leu	Ser	Trp	Ala
225				230						235					240
Asp	Pro	Gln	Gly	Ile	Asn	Val	Arg	Leu	Arg	Ala	Ala	Arg	Asn	Ala	Leu
				245					250					255	
Asp	Glu	Phe	Ile	Asp	Lys	Ile	Ile	Asp	Glu	His	Met	Glu	Arg	Gly	Lys
		260						265					270		
Asn	Pro	Asp	Asp	Ala	Asp	Ala	Asp	Met	Val	Asp	Asp	Met	Leu	Ala	Phe
		275					280					285			
Leu	Pro	Glu	Ala	Lys	Pro	Lys	Lys	Gly	Ala	Ala	Gly	Asp	Gly	Val	Asp
	290					295					300				
Asp	Leu	Gln	Asn	Thr	Leu	Arg	Leu	Thr	Arg	Asp	Asn	Ile	Lys	Ala	Ile
305					310					315					320
Ile	Met	Asp	Val	Met	Phe	Gly	Gly	Thr	Glu	Thr	Val	Ala	Ser	Ala	Ile
				325					330					335	
Glu	Trp	Ala	Met	Ala	Glu	Met	Met	His	Ser	Pro	Asp	Asp	Leu	Arg	Arg
		340						345					350		
Leu	Gln														

435					440					445						
Ala	Gly	Leu	Asp	Phe	Lys	Gly	Gly	Cys	Phe	Glu	Phe	Leu	Pro	Phe	Gly	
450					455					460						
Ser	Gly	Arg	Arg	Ser	Cys	Pro	Gly	Met	Ala	Leu	Gly	Leu	Tyr	Ala	Leu	
465					470					475					480	
Glu	Leu	Ala	Val	Ala	Gln	Leu	Ala	His	Gly	Phe	Ser	Trp	Glu	Leu	Pro	
485					490					495					500	
Asp	Gly	Met	Lys	Pro	Ser	Glu	Leu	Asp	Met	Ser	Asp	Val	Phe	Gly	Leu	
500					505					510					515	
Thr	Ala	Pro	Arg	Ala	Thr	Arg	Leu	Phe	Ala	Val	Pro	Thr	Pro	Arg	Leu	
515					520					525					530	
Ala	Cys	Thr	Gln	Leu	Leu	Gly	Ala	Asp	Asp	Ala	Gly	Arg	Gln	Ala		
530					535					540						

<210> 184

<211> 713

<212> PRT

<213> Festuca arundinacea

<400> 184

Met	Glu	Cys	Glu	Asn	Gly	His	Val	Ala	Ala	Asn	Gly	Asp	Gly	Leu	Cys
1				5					10					15	
Val	Ala	Gln	Pro	Ala	Arg	Ala	Asp	Pro	Leu	Asn	Trp	Gly	Lys	Ala	Ala
			20					25					30		
Glu	Glu	Leu	Ser	Gly	Ser	His	Leu	Asp	Ala	Val	Lys	Arg	Met	Val	Glu
		35					40					45			
Glu	Tyr	Arg	Arg	Pro	Val	Val	Thr	Met	Glu	Gly	Ala	Ser	Leu	Thr	Ile
	50					55					60				
Ala	Met	Val	Ala	Ala	Val	Ala	Ala	Gly	Ala	Asp	Thr	Arg	Val	Glu	Leu
65					70				75					80	
Asp	Glu	Ser	Ala	Arg	Gly	Arg	Val	Lys	Glu	Ser	Ser	Asp	Trp	Val	Met
				85				90						95	
Asn	Ser	Met	Ala	Asn	Gly	Thr	Asp	Ser	Tyr	Gly	Val	Thr	Thr	Gly	Phe
		100						105					110		
Gly	Ala	Thr	Ser	His	Arg	Arg	Thr	Lys	Glu	Gly	Gly	Ala	Leu	Gln	Arg
		115					120					125			
Glu	Leu	Ile	Arg	Phe	Leu	Asn	Ala	Gly	Ala	Phe	Gly	Thr	Gly	Ser	Asp
	130					135					140				
Gly	His	Val	Leu	Pro	Ala	Ala	Thr	Thr	Arg	Ala	Ala	Met	Leu	Val	Arg
145					150				155					160	
Val	Asn	Thr	Leu	Leu	Gln	Gly	Tyr	Ser	Gly	Ile	Arg	Phe	Glu	Ile	Leu
			165						170					175	
Glu	Thr	Ile	Ala	Thr	Leu	Leu	Asn	Ala	Asn	Val	Thr	Pro	Cys	Leu	Pro
		180					185						190		
Leu	Arg	Gly	Thr	Ile	Thr	Ala	Ser	Gly	Asp	Leu	Val	Pro	Leu	Ser	Tyr
	195					200						205			
Ile	Ala	Gly	Leu	Val	Thr	Gly	Arg	Pro	Asn	Ser	Val	Ala	Thr	Ala	Pro
	210					215					220				
Asp	Gly	Ser	Lys	Val	Asn	Ala	Ala	Glu	Ala	Phe	Lys	Ile	Ala	Gly	Ile
225					230				235					240	
Gln	His	Gly	Phe	Phe	Glu	Leu	Gln	Pro	Lys	Glu	Gly	Leu	Ala	Met	Val
			245						250					255	
Asn	Gly	Thr	Ala	Val	Gly	Ser	Gly	Leu	Ala	Ser	Ile	Val	Leu	Phe	Glu
		260					265						270		
Ala	Asn	Ile	Leu	Gly	Ile	Leu	Ala	Glu	Val	Leu	Ser	Ala	Val	Phe	Cys
	275					280						285			
Glu	Val	Met	Asn	Gly	Lys	Pro	Glu	Tyr	Thr	Asp	His	Leu	Thr	His	Lys
	290					295					300				
Leu	Lys	His	His	Pro	Gly	Gln	Ile	Glu	Ala	Ala	Ala	Ile	Met	Glu	His
305					310				315					320	
Ile	Leu	Glu	Gly	Ser	Ser	Tyr	Met	Met	Leu	Ala	Lys	Lys	Leu	Gly	Glu
			325						330					335	
Leu	Asp	Pro	Leu	Met	Lys	Pro	Lys	Gln	Asp	Arg	Tyr	Ala	Leu	Arg	Thr
		340					345					350			
Ser	Pro	Gln	Trp	Leu	Gly	Pro	Gln	Ile	Glu	Val	Ile	Arg	Ala	Ala	Thr
		355					360					365			

Lys Ser Ile Glu Arg Glu Ile Asn Ser Val Asn Asp Asn Pro Leu Ile
 370 375 380
 Asp Val Ser Arg Gly Lys Ala Ile His Gly Gly Asn Phe Gln Gly Thr
 385 390 395 400
 Pro Ile Gly Val Ser Met Asp Asn Thr Arg Leu Ala Ile Ala Ala Ile
 405 410 415
 Gly Lys Leu Met Phe Ala Gln Phe Ser Glu Leu Val Asn Asp Phe Tyr
 420 425 430
 Asn Asn Gly Leu Pro Ser Asn Leu Ser Gly Gly Arg Asn Pro Ser Leu
 435 440 445
 Asp Tyr Gly Phe Lys Gly Ala Glu Ile Ala Met Ala Ser Tyr Cys Ser
 450 455 460
 Glu Leu Gln Phe Leu Gly Asn Pro Val Thr Asn His Val Gln Ser Ala
 465 470 475 480
 Glu Gln His Asn Gln Asp Val Asn Ser Leu Gly Leu Ile Ser Ser Arg
 485 490 495
 Lys Thr Ala Glu Ala Ile Asp Ile Leu Lys Leu Met Ser Ser Thr Phe
 500 505 510
 Met Val Ala Leu Cys Gln Ala Ile Asp Leu Arg His Ile Glu Glu Asn
 515 520 525
 Val Lys Asn Ala Val Lys Asn Cys Val Lys Thr Val Ala Arg Lys Thr
 530 535 540
 Leu Ser Thr Asn Asp Ser Gly His Leu His Asn Ala Arg Phe Cys Glu
 545 550 555 560
 Lys Asp Leu Leu Leu Thr Ile Asp Arg Glu Ala Val Phe Ala Tyr Ala
 565 570 575
 Asp Asp Pro Cys Ser Ala Asn Tyr Pro Leu Met Gln Lys Met Arg Ala
 580 585 590
 Val Leu Val Glu His Ala Leu Ala Asn Gly Glu Ala Glu Gln Asp Val
 595 600 605
 Gln Thr Ser Val Phe Ala Lys Leu Ala Thr Phe Glu Gln Glu Leu Arg
 610 615 620
 Ala Val Leu Pro Lys Glu Val Glu Ser Ala Arg Cys Ser Val Glu Asn
 625 630 635 640
 Gly Thr Ala Ala Gln Gln Asn Arg Ile Ser Glu Cys Arg Ser Tyr Pro
 645 650 655
 Leu Tyr Arg Phe Val Arg Lys Glu Leu Gly Thr Glu Tyr Leu Thr Gly
 660 665 670
 Glu Lys Thr Arg Ser Pro Gly Glu Glu Val Asp Lys Val Phe Val Ala
 675 680 685
 Met Asn Gln Gly Lys His Ile Asp Ala Leu Leu Glu Cys Leu Lys Glu
 690 695 700
 Trp Asn Gly Glu Pro Leu Pro Ile Cys
 705 710

<210> 185

<211> 324

<212> PRT

<213> Lolium perenne

<400> 185

Met Ala Pro Ala Thr Pro Lys Asp Ser Ser Ala Leu Pro Gly Leu Leu
 1 5 10 15
 Leu Leu Phe Ala Ala Ala Thr Ser Val Ala Val Ala Asn Ala Gln Leu
 20 25 30
 Ser Glu Asn Tyr Tyr Gly Ser Ser Cys Pro Thr Ala Leu Thr Ile
 35 40 45
 Arg Thr Val Val Thr Thr Ala Val Leu Leu Asp His Arg Met Gly Ala
 50 55 60
 Ser Leu Leu Arg Leu His Phe His Asp Cys Phe Val Gln Gly Cys Asp
 65 70 75 80
 Ala Ser Val Leu Leu Asp Asp Thr Ala Gly Phe Thr Gly Glu Lys Gly
 85 90 95
 Ala Gly Pro Asn Ala Gly Ser Leu Arg Gly Leu Glu Val Ile Asp Lys
 100 105 110
 Ile Lys Met Leu Leu Glu Phe Met Cys Pro Arg Thr Val Ser Cys Ala

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      115      120      125
Asp Ile Leu Ala Val Ala Ala Arg Asp Ser Val Val Arg Leu Gly Gly
 130      135      140
Pro Ser Trp Ala Val Gln Leu Gly Arg Arg Asp Ala Thr Thr Ala Ser
145      150      155      160
Ala Ser Leu Ala Ser Ser Asp Leu Pro Gly Pro Asn Ser Asn Leu Asn
      165      170      175
Asp Leu Leu Thr Ala Phe Ser Lys Lys Gly Leu Ser Thr Thr Asp Met
      180      185      190
Val Ala Leu Ser Gly Ala His Thr Ile Gly Arg Ala Gln Cys Gln Asn
      195      200      205
Tyr Arg Asn Arg Ile Tyr Thr Asp Thr Asp Ile Asp Gly Ala Phe Ala
 210      215      220
Ala Ser Leu Arg Gly Gly Cys Pro Gln Ala Gly Gly Asp Gly Asn Leu
225      230      235      240
Ala Pro Leu Asp Ala Ser Ser Pro Asn Thr Phe Asp Asn Gly Tyr Phe
      245      250      255
Ser Gly Leu Leu Ser Arg Gln Gly Leu Leu His Ser Asp Gln Ala Leu
      260      265      270
Tyr Asp Gly Gly Ser Thr Asp Asp Leu Val Arg Thr Tyr Ala Ser Asn
      275      280      285
Asn Asp Gln Phe Gly Ser Asp Phe Ala Ala Ala Met Val Lys Leu Ser
      290      295      300
Asn Ile Gly Leu Leu Thr Gly Ser Ser Gly Glu Ile Arg Val Asn Cys
305      310      315      320
Arg Ala Val Asn

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<210> 186

<211> 398

<212> PRT

<213> Lolium perenne

<400> 186

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Met Ala Ala Thr Met Thr Val Glu Glu Val Arg Lys Ala Gln Arg Ala
 1      5      10      15
Glu Gly Pro Ala Thr Val Leu Ala Ile Gly Thr Ala Thr Pro Ala Asn
      20      25      30
Cys Val Tyr Gln Ala Asp Tyr Pro Asp Tyr Tyr Phe Lys Ile Thr Lys
      35      40      45
Ser Asp His Leu Ala Asp Leu Lys Glu Lys Phe Lys Arg Met Cys Asp
      50      55      60
Lys Ser Gln Ile Arg Lys Arg Tyr Met His Leu Thr Glu Glu Ile Leu
      65      70      75      80
Glu Glu Asn Pro Asn Met Cys Ala Tyr Met Ala Pro Ser Leu Asp Ala
      85      90      95
Arg Gln Asp Ile Val Val Val Glu Val Pro Lys Leu Gly Lys Ala Ala
      100      105      110
Ala Gln Lys Ala Ile Lys Glu Trp Gly Gln Pro Arg Ser Lys Ile Thr
      115      120      125
His Leu Val Phe Cys Thr Thr Ser Gly Val Asp Met Pro Gly Ala Asp
      130      135      140
Tyr Gln Leu Thr Lys Met Leu Gly Leu Arg Pro Ser Val Lys Arg Leu
      145      150      155      160
Met Met Tyr Gln Gln Gly Cys Phe Ala Gly Gly Thr Val Leu Arg Leu
      165      170      175
Ala Lys Asp Leu Ala Glu Asn Asn Arg Gly Ala Arg Val Leu Val Val
      180      185      190
Cys Ser Glu Ile Thr Ala Val Thr Phe Arg Gly Pro His Glu Ser His
      195      200      205
Leu Asp Ser Leu Val Gly Gln Ala Leu Phe Gly Asp Gly Ala Ala Ala
      210      215      220
Val Ile Ile Gly Ala Asp Pro Asp Val Ser Val Glu Arg Pro Leu Phe
      225      230      235      240
Gln Leu Val Ser Ala Ser Gln Thr Ile Leu Pro Asp Ser Glu Gly Ala
      245      250      255

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Ile Asp Gly His Leu Arg Glu Val Gly Leu Thr Phe His Leu Leu Lys
      260      265      270
Asp Val Pro Gly Leu Ile Ser Lys Asn Ile Glu Arg Ala Leu Glu Glu
      275      280      285
Ala Phe Lys Pro Leu Gly Ile Asp Asp Trp Asn Ser Val Phe Trp Val
      290      295      300
Ala His Pro Gly Gly Pro Ala Ile Leu Asp Met Val Glu Ala Lys Val
      305      310      315      320
Asn Leu Asn Lys Glu Arg Met Arg Ala Thr Arg His Val Leu Ser Glu
      325      330      335
Tyr Gly Asn Met Ser Ser Ala Cys Val Leu Phe Ile Met Asp Glu Met
      340      345      350
Arg Lys Arg Ser Ala Glu Asp Gly His Thr Thr Thr Gly Glu Gly Met
      355      360      365
Asp Trp Gly Val Leu Phe Gly Phe Gly Pro Gly Leu Thr Val Glu Thr
      370      375      380
Val Val Leu His Ser Met Pro Ile Ala Ala Asp Ala Thr Ala
      385      390      395

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<210> 187

<211> 370

<212> PRT

<213> Festuca arundinacea

<400> 187

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Met Lys Gln Glu Val Lys Ser Glu Met Asn Gly Glu Thr Met Ser Gly
  1      5      10      15
Asn Lys Gly Pro Val Val Val Thr Gly Ala Ser Gly Phe Val Gly Ser
      20      25      30
Trp Leu Val Met Lys Leu Leu Gln Ala Gly Tyr Thr Val Arg Ala Thr
      35      40      45
Val Arg Asp Pro Gly Asn Val Glu Lys Thr Lys Pro Leu Leu Glu Leu
      50      55      60
Pro Gly Ala Lys Glu Arg Leu Ser Ile Trp Arg Ala Asp Leu Ser Glu
      65      70      75      80
Glu Gly Ser Phe Asp Glu Ala Ile Ala Gly Cys Thr Gly Val Phe His
      85      90      95
Val Ala Thr Pro Met Asp Phe Glu Ser Lys Asp Pro Glu Asn Glu Val
      100      105      110
Ile Lys Pro Thr Val Glu Gly Met Leu Ser Ile Met Arg Ala Cys Lys
      115      120      125
Glu Ala Gly Thr Val Lys Arg Val Val Phe Thr Ser Ser Ala Gly Thr
      130      135      140
Val Asn Ile Glu Glu Arg Pro Arg Pro Ala Tyr Asp Gln Asp Asn Trp
      145      150      155      160
Ser Asp Ile Asp Phe Cys Arg Arg Val Lys Met Thr Gly Gln Met Tyr
      165      170      175
Phe Val Ser Lys Ser Leu Ala Glu Lys Ala Ala Met Asp Tyr Ala Lys
      180      185      190
Glu Asn Gly Val Asp Phe Ile Ser Ile Ile Pro Thr Leu Val Val Gly
      195      200      205
Pro Phe Leu Ser Ala Gly Met Pro Pro Ser Leu Val Thr Ala Leu Ala
      210      215      220
Leu Ile Thr Gly Asn Glu Ala His Tyr Ser Ile Leu Lys Gln Val Gln
      225      230      235      240
Leu Val His Leu Asp Asp Leu Cys Asp Ser Met Thr Tyr Leu Phe Glu
      245      250      255
His Pro Asp Ala Asn Gly Arg Tyr Ile Cys Ser Ser His Asp Thr Thr
      260      265      270
Ile His Gly Ile Ala Arg Met Leu Lys Glu Arg Phe Pro Glu Tyr Asp
      275      280      285
Ile Pro Gln Lys Phe Pro Gly Val Asp Asp Asp Leu Gln Pro Ile His
      290      295      300
Phe Phe Phe Lys Lys Leu Leu Asp His Gly Phe Arg Phe Arg Tyr Thr
      305      310      315      320
Ala Glu Asp Met Phe Asp Ala Ala Val Trp Thr Cys Arg Glu Lys Gly

```

325 330 335
 Leu Ile Pro Leu Gly Ala Glu Gly Ala Gly Gly Pro Ala Ser Ala Ala
 340 345 350
 Gly Lys Leu Gly Ala Val Leu Val Gly Glu Gly Gln Ala Ile Gly Ala
 355 360 365
 Glu Thr
 370

<210> 188
 <211> 329
 <212> PRT
 <213> Lolium perenne

<400> 188
 Met Ala Thr Glu Ala Lys Gly Glu Thr Val Leu Val Thr Gly Ala Ser
 1 5 10 15
 Gly Phe Ile Gly Ser Trp Leu Val Arg Leu Leu Leu Ala Arg Gly Tyr
 20 25 30
 Ser Val His Ala Ala Val Leu Asn Pro Asp Asp Lys Ala Glu Thr Asp
 35 40 45
 His Leu Leu Ala Leu Ala Ala Ala Gly Asp Glu Gly Arg Ile Arg
 50 55 60
 Phe Phe Arg Cys Asp Leu Leu Asp Gly Ala Ala Met Leu Ala Ala Val
 65 70 75 80
 Arg Gly Cys Ser Gly Val Phe His Leu Ala Ser Pro Cys Thr Val Asp
 85 90 95
 Leu Val Leu Asp Pro Gln Lys Glu Leu Val Val Pro Ala Val Glu Gly
 100 105 110
 Thr Leu Asn Val Leu Arg Ala Ala Lys Glu Ala Gly Gly Val Arg Arg
 115 120 125
 Val Val Val Thr Ser Ser Val Ser Ala Leu Val Pro Cys Pro Gly Trp
 130 135 140
 Pro Ala Gly Glu Val Leu Asp Glu Arg Cys Trp Thr Asp Ile Asp Tyr
 145 150 155 160
 Cys Asp Lys Asn Gly Val Trp Tyr Pro Ala Ser Lys Ala Leu Ala Glu
 165 170 175
 Lys Ala Ala Trp Lys Phe Ala Glu Glu Asn Gly Leu Asp Val Val Thr
 180 185 190
 Val Asn Pro Gly Thr Val Leu Gly Glu Met Ile Pro Pro Arg Leu Asn
 195 200 205
 Ala Ser Met Ala Met Phe Leu Arg Leu Leu Glu Gly Cys Lys Glu Glu
 210 215 220
 Tyr Ala Asp Phe Phe Ile Gly Pro Val His Val Glu Asp Val Ala Leu
 225 230 235 240
 Ala His Ile Leu Leu Tyr Glu Asn Pro Ser Ala Ser Gly Arg His Leu
 245 250 255
 Cys Val Glu Pro Ile Cys His Trp Ser Val Phe Ala Ala Lys Val Ala
 260 265 270
 Glu Leu Tyr Pro Asp Tyr Lys Val Pro Lys Phe Pro Glu Asp Thr Gln
 275 280 285
 Pro Gly Leu Val Arg Ala Glu Ala Val Pro Lys Lys Leu Met Ala Leu
 290 295 300
 Gly Leu Gln Phe Thr Pro Leu Glu Lys Ile Ile Arg Asp Ala Val Glu
 305 310 315 320
 Ser Leu Lys Ser Arg Gly Cys Ile Ala
 325

<210> 189
 <211> 330
 <212> PRT
 <213> Lolium perenne

<400> 189
 Met Val Ser Ser Thr Lys Gly Lys Val Cys Val Thr Gly Ala Ser Gly
 1 5 10 15
 Phe Val Ala Ser Trp Leu Ile Lys Lys Leu Leu Glu Ser Gly Tyr His

<400>	190														
Met	Ala	Pro	Ala	Thr	Pro	Lys	Asp	Ser	Ser	Ser	Ser	Ala	Leu	Pro	Gly
1				5					10					15	
Leu	Leu	Leu	Leu	Leu	Ala	Ala	Ala	Thr	Ser	Val	Ala	Val	Ala	Asn	Ala
.			20					25					30		
Gln	Leu	Ser	Glu	Asn	Tyr	Tyr	Gly	Ser	Ser	Cys	Pro	Thr	Ala	Leu	Leu
		35				40						45			
Thr	Ile	Arg	Thr	Val	Val	Thr	Thr	Ala	Val	Leu	Leu	Asp	His	Arg	Met
	50					55					60				
Gly	Ala	Ser	Leu	Leu	Arg	Leu	His	Phe	His	Asp	Cys	Phe	Val	Gln	Gly
65					70					75					80
Cys	Asp	Ala	Ser	Val	Leu	Leu	Asp	Asp	Thr	Ala	Gly	Phe	Thr	Gly	Glu
				85					90					95	
Lys	Gly	Ala	Gly	Pro	Asn	Ala	Gly	Ser	Leu	Arg	Gly	Leu	Glu	Val	Ile
			100					105					110		
Asp	Lys	Ile	Lys	Met	Leu	Leu	Glu	Phe	Met	Cys	Pro	Arg	Thr	Val	Ser
		115					120					125			
Cys	Ala	Asp	Ile	Leu	Ala	Val	Ala	Ala	Arg	Asp	Ser	Val	Val	Arg	Leu
	130					135					140				
Gly	Gly	Pro	Ser	Trp	Ala	Val	Gln	Leu	Gly	Arg	Arg	Asp	Ala	Thr	Thr
145				150						155					160

Ala Ser Ala Ser Leu Ala Ser Ser Asp Leu Pro Gly Pro Asn Ser Asn
 165 170 175
 Leu Asn Asp Leu Leu Thr Ala Phe Ser Lys Lys Gly Leu Ser Thr Thr
 180 185 190
 Asp Met Val Ala Leu Ser Gly Ala His Thr Ile Gly Arg Ala Gln Cys
 195 200 205
 Gln Asn Tyr Arg Asn Arg Ile Tyr Thr Asp Thr Asp Ile Asp Gly Ala
 210 215 220
 Phe Ala Ala Ser Leu Arg Gly Gly Cys Pro Gln Ala Gly Gly Asp Gly
 225 230 235 240
 Asn Leu Ala Pro Leu Asp Ala Ser Ser Pro Asn Thr Phe Asp Asn Gly
 245 250 255
 Tyr Phe Ser Gly Leu Leu Ser Arg Gln Gly Leu Leu His Ser Asp Gln
 260 265 270
 Ala Leu Tyr Asp Gly Gly Ser Thr Asp Asp Leu Val Arg Thr Tyr Ala
 275 280 285
 Ser Asn Asn Asp Gln Phe Gly Ser Asp Phe Ala Ala Met Val Lys
 290 295 300
 Leu Ser Asn Ile Gly Leu Leu Thr Gly Ser Ser Gly Glu Ile Arg Val
 305 310 315 320
 Asn Cys Arg Ala Val Asn
 325

<210> 191
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Made in the lab

<400> 191
 catatggata agctcaatgg ttctgc

26

<210> 192
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Made in the lab

<400> 192
 cggtagagat ccagtctaga g

21

<210> 193
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Made in the lab

<400> 193
 tacatatgct gcacgagaag ttctacag

28

<210> 194
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Made in the lab

<400> 194
ccacggctaa ctaatggttc a 21

<210> 195
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in the lab

<400> 195
tacatatgaa aggttctggg ctgtccgtc 29

<210> 196
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in the lab

<400> 196
ctagttcacc ttggagcagt tg 22

<210> 197
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in the lab

<400> 197
gcagacggcg gtctactt 18

<210> 198
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in the lab

<400> 198
aaatgcaagt gacccaacgt tac 23

<210> 199
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in the lab

<400> 199
tcatgacgat tccaagaacg 20

<210> 200
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in the lab

<400> 200
gttgaccgtg actcgtcgt 19

<210> 201
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in the lab

<400> 201
actgaattct cgggtcccagc ctccatt 27

<210> 202
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in the lab

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